COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN *FEZ1* GENE, A NOVEL TUMOR SUPPRESSOR GENE

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is entitled to priority pursuant to 35 U.S.C. §119(e) to U.S. provisional patent application 60/121,537 which was filed on February 25, 1999.

STATEMENT REGARDING FEDERALLY SUPPORTED RESEARCH AND DEVELOPMENT

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BACKGROUND OF THE INVENTION

The invention relates generally to cancer and tumor suppressor genes.

Proliferation of normal cells is thought to be regulated by growth-promoting proto-oncogenes and by growth-constraining tumor suppressor genes (Weinberg, 1991, Science 254:1138). Genetic alterations that inactivate tumor suppressor genes or that activate proto-oncogenes free cells from growth constraints imposed by the non-altered genes, thereby enabling tumor growth. Accumulation of genetic aberrations in a cell *in vivo* causes the cell to proceed from a normal growth or quiescent stage, potentially through a discernable pre-neoplastic stage, to a cancerous stage in which the cell replicates abnormally quickly, and potentially spreads to body locations at which the cell is not normally found (Knudson, 1993, Proc. Natl. Acad. Sci. USA 90:10914; Nowell, 1993, Adv. Cancer Res. 62:1).

The presence of a tumor suppressor gene at a particular chromosomal location is sometimes evidenced by an increased prevalence of loss of heterozygosity

(LOH) at the chromosomal location in tumor tissues, relative to non-cancerous tissue (Weinberg, 1991, Science 254:1138; Lasko et al., 1991, Ann. Rev. Genet. 25:281; Knudson, 1993, Proc. Natl. Acad. Sci. USA 90:10914; Nowell, 1993, Adv. Cancer Res. 62:1). Allelotyping studies indicate that allelic loss(es) on chromosome 8p, particularly at band 21-22, are associated with various tumors, including prostate tumors, breast tumors, head and neck squamous cell carcinomas, urinary bladder carcinomas, hepatocellular carcinomas, and hematological malignancies (Kagan et al., 1995, Oncogene 11:2121; Macoska et al., 1995, Cancer Res. 55:5390; Jenkins et al., 1998, Genes Chromosom. Cancer 21:131; Yaremko et al., 1995, Genes Chromosom. Cancer 13:186; Yaremko et al., 1996, Genes Chromosom. Cancer 16:189; Kerangueven et al., 1997, Cancer Res. 57:5469; Anbazhagan et al., 1998, Am. J. Pathol. 152:815; El-Naggar et al., 1998, Oncogene 16:2983; Sunwoo et al., 1996, Genes Chromosom. Cancer 16:164; Wu et al., 1997, Genes Chromosom. Cancer 20:347; Wagner et al., 1997, Am. J. Pathol. 151:753; Boige et al., 1997, Cancer Res. 57:1986; Takeuchi et al., 1995, Cancer Res. 55:5377).

Studies in which chromosome regions were transferred into tumor cells have provided evidence that one or more tumor suppressor genes is present at human chromosome location 8p (Gustafson et al., 1996, Cancer Res. 56:5238; Ichikawa et al., 1994, Cancer Res. 54:2299; Kuramochi et al., 1997, Prostate 31:14). These observations suggest that chromosome region 8p21-22 has an important role in the development of various tumors.

Efforts by others to identify tumor suppressor gene(s) located on chromosome 8p identified two candidate tumor suppressor genes, designated *N33* and *PRLTS* (Bookstein et al., 1997, Br. J. Urol. 79(Suppl. 1):28; Bova et al., 1996, Genomics 35:46; MacGrogan et al., 1996, Genomics 35:55; Cher et al., 1994, Genes Chromosom. Cancer 11:153; Bookstein, et al., 1994, Genomics 24:317; Fujiwara et al., 1995, Oncogene 10:891; Komiya et al., 1997, Jpn. J. Cancer Res. 88:389). Gene *N33* is located at position 8p22, near the *MSR* gene locus, but no point mutations in *N33* have been associated with tumors. Four cancer-associated point mutations have been

reported in *PRLTS*, which is located at position 8p21.3-22. The frequency of alterations in this gene was, however, very low. Thus, it is unlikely that either the *N33* gene or the *PRLTS* gene are tumor suppressor genes associated with common cancers.

Until the present disclosure, the tumor suppressor gene(s) located at chromosome location 8p has not been identified. The failure of others to identify this gene has delayed development of diagnostic, therapeutic, and other useful methods and compositions which involve this tumor suppressor gene. The present invention enables these methods and compositions.

BRIEF SUMMARY OF THE INVENTION

The invention relates to an isolated polynucleotide comprising a portion which anneals with high stringency with (i.e. is substantially complementary to) 20 or more, consecutive nucleotide residues of a strand of a human *FEZ1* gene. An exemplary human *FEZ1* gene has the nucleotide sequence SEQ ID NO: 1. The portion which anneals can be substantially homologous with the residues of the human *FEZ1* gene or, preferably, it can be completely homologous with those residues. Preferably, the portion is at least substantially homologous with at least twenty residues of an exon region of the human *FEZ1* gene, i.e. nucleotide residues 112-456, nucleotide residues 1707-2510, and nucleotide residues 4912-5550 of a strand of SEQ ID NO: 1.

In one embodiment, the isolated polynucleotide of the invention comprises a portion having the nucleotide sequence of a strand of SEQ ID NO: 3, and optionally further comprises a promoter. The promoter may, for example, be a constitutive promoter, an inducible promoter, or a tissue-specific promoter.

In another embodiment of the isolated polynucleotide of the invention, the isolated polynucleotide is incorporated in a nucleic acid vector or is encoded by nucleic acid which is incorporated in a nucleic acid vector. The isolated polynucleotide may, for example, have a sequence homologous with a strand of SEQ ID NO: 1, and it can be detectably labeled. Examples of detectably labeled isolated polynucleotides include immobilized polynucleotides, polynucleotides linked to a protein of a protein-

ligand pair, polynucleotides linked to a ligand of a protein-ligand pair, biotinylated polynucleotides, polynucleotides linked to a fluorophore, polynucleotides linked to a chromophore, polynucleotides linked to an enzyme, and radio-labeled polynucleotides. When an immobilized polynucleotide is used, it can be immobilized on the surface of a gene chip. Preferably, the isolated polynucleotide of the invention is substantially purified.

The isolated polynucleotide of the invention need not comprise only naturally occurring bases and linkages. It may, for example, have at least two nucleotide residues linked by a non-naturally occurring linkage other than a phosphodiester linkage such as, for example, a linkage selected from the group consisting of phosphonate, phosphorothioate, phosphorodithioate, phosphoramidate methoxyethyl phosphoramidate, formacetal, thioformacetal, diisopropylsilyl, acetamidate, carbamate, dimethylene-sulfide ($-CH_2-S-CH_2-$), dimethylene-sulfoxide ($-CH_2-SO-CH_2-$), dimethylene-sulfone ($-CH_2-SO_2-CH_2-$), 2'-O-alkyl, and 2'-deoxy-2'-fluoro phosphorothioate, phosphotriester, siloxane, carbonate, carboxymethyl ester, acetamidate, thioether, bridged phosphoramidate, bridged methylene phosphonate, bridged phosphoramidate, bridged phosphoramidate, bridged methylene phosphonate, phosphorothioate, methylphosphonate, phosphorodithioate, bridged phosphorothioate linkages, bridged sulfone linkages, and combinations of such linkages. Furthermore, an end of the isolated polynucleotide can be nucleolytically blocked.

The invention also includes an isolated polynucleotide comprising a portion which has a sequence which anneals with high stringency with at least twenty consecutive nucleotide residues of a strand of SEQ ID NO: 3.

In another aspect, the invention includes a kit for amplifying a portion of a human *FEZ1* gene. The kit comprises a first isolated polynucleotide and a second isolated polynucleotide. The first isolated polynucleotide comprises a portion which anneals with high stringency with at least twenty consecutive nucleotide residues of the coding strand of SEQ ID NO: 1, and the second isolated polynucleotide comprises a

portion which anneals with high stringency with at least twenty consecutive nucleotide residues of the non-coding strand of SEQ ID NO: 1.

The invention further includes a kit for amplifying a portion of a cDNA generated from a transcript of a human *FEZ1* gene. The kit comprises a first isolated polynucleotide and a second isolated polynucleotide. A portion of the first isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the coding strand of SEQ ID NO: 1, and a portion of the second isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the non-coding strand of SEQ ID NO: 1.

Furthermore, the invention includes an animal cell comprising an exogenous DNA molecule having a portion substantially homologous with at least nucleotide residues 112-456, nucleotide residues 1707-2510, and nucleotide residues 4912-5550 of a strand of SEQ ID NO: 1. In one embodiment, the exogenous DNA molecule further comprises a promoter operably linked with the portion, and the exogenous DNA molecule is expressed in the animal cell.

The invention also includes a genetically altered animal comprising a cell into which an exogenous DNA molecule has been artificially introduced. The exogenous DNA molecule has a portion substantially homologous with at least the coding region of a strand of a human *FEZ1* gene. The exogenous DNA molecule may, for example, have a portion substantially homologous with at least nucleotide residues 112-456, nucleotide residues 1707-2510, and nucleotide residues 4912-5550 of a strand of SEQ ID NO: 1, or it can comprise a portion having a sequence substantially homologous with a strand of SEQ ID NO: 2.

The invention also relates to an isolated human Fez1 protein, such as a protein having an amino acid sequence substantially, or preferably completely, homologous with SEQ ID NO: 4. In one embodiment, the protein is substantially purified.

The invention further includes an isolated antibody which binds specifically with human Fezl protein and a hybridoma cell which produces such antibodies.

The invention still further relates to a method of determining the cancerous status of a sample tissue. This method comprises comparing *FEZ1* expression in the sample tissue with *FEZ1* expression in a control tissue of the same type. Decreased *FEZ1* expression in the sample tissue, relative to *FEZ1* expression in the control tissue, is an indication that the sample tissue is cancerous. In one embodiment, the sample tissue is a phenotypically abnormal portion of a body tissue of a human, and the control tissue is a phenotypically normal portion of the body tissue, such as an epithelial tissue. The body tissue can also, for example, be selected from the group consisting of a gastrointestinal tissue, esophagus tissue, gastric tissue, colon tissue, prostate tissue, breast tissue, a hematopoietic tissue, lung tissue, melanoma tissue, cervical tissue, and ovarian tissue. In an alternative embodiment of this method, *FEZ1* expression in the sample tissue is compared with *FEZ1* expression in the control tissue by comparing the relative amounts of an indicator in the sample tissue and in the control tissue. The indicator may, for example, be selected from the group consisting of a *FEZ1* mRNA, a cDNA prepared using a *FEZ1* mRNA, a DNA prepared by amplification of either of these, and Fezl protein.

The invention also includes a method of determining the cancerous status of a sample tissue. This method comprises comparing the nucleotide sequence of a *FEZ1*-associated polynucleotide obtained from the sample tissue with the nucleotide sequence of a control *FEZ1*-associated polynucleotide. A difference between the nucleotide sequence of the *FEZ1*-associated polynucleotide obtained from the sample tissue and the nucleotide sequence of the control *FEZ1*-associated polynucleotide is an indication that the sample tissue is cancerous.

The invention includes another method of determining the cancerous status of a human sample tissue. This method comprises comparing the length of an *FEZ1*-transcript-associated polynucleotide obtained from the sample tissue with the

length of a control *FEZ1*-transcript-associated polynucleotide. If the length of the *FEZ1*-transcript-associated polynucleotide obtained from the sample tissue is less than the length of the control *FEZ1*-transcript-associated polynucleotide, then this is an indication that the sample tissue is cancerous.

The invention includes yet another method of determining the cancerous status of a sample tissue. This method comprises assessing *FEZ1* expression in the sample tissue. A substantial absence of *FEZ1* expression in the sample tissue is an indication that the sample tissue is cancerous. *FEZ1* expression can be assessed, for example, by assessing the presence or substantial absence of an indicator selected from the group consisting of a *FEZ1* mRNA, a cDNA prepared using a *FEZ1* mRNA, a DNA prepared by amplification of either of these, and Fez1 protein.

The invention includes yet another method of determining the cancerous status of a sample tissue. This method comprises detecting abnormal splicing of a *FEZ1* transcript in the sample tissue. Abnormal splicing of the *FEZ1* transcript is an indication that the sample tissue is cancerous. Abnormal splicing of the *FEZ1* transcript can be detected, for example, by assessing the ability of an exon boundary polynucleotide probe to anneal with a *FEZ1*-transcript-associated polynucleotide with high stringency. The exon boundary polynucleotide probe is capable of annealing with high stringency with terminal portions of two sequential *FEZ1* exons when the terminal portions are adjacent, but not when the terminal portions are not adjacent.

In another aspect, the invention relates to a method of modulating abnormal proliferation of a human cell having an altered *FEZ1* gene. This method comprises providing an exogenous source of Fez1 protein to the cell. Abnormal proliferation of the cell is thereby inhibited, delayed, or prevented. The exogenous source of Fez1 protein may, for example, be a composition comprising an isolated human Fez1 protein, such as a human Fez1 protein having the amino acid sequence SEQ ID NO: 4. The exogenous source of Fez1 protein can also be an expression vector (e.g. an adenovirus vector, such as one comprising a vector nucleic acid having the nucleotide sequence SEQ ID NO: 60) comprising a polynucleotide having a coding

region which encodes a functional Fez1 protein, such as a human *FEZ1* gene having the nucleotide sequence of a strand of SEQ ID NO: 3. The polynucleotide can further comprise a constitutive, inducible, or tissue-specific promoter operably linked with the coding region. When the promoter is an inducible promoter, the method further comprises administering an inducer of the inducible promoter to the cell. The polynucleotide may, of course, comprise a wild-type *FEZ1* promoter region.

In still another aspect, the invention relates to a method of preventing tumorigenesis in a human cell. This method comprises providing to the cell an expression vector comprising a polynucleotide having a coding region which encodes a functional Fez1 protein. Upon providing the expression vector to the cell, tumorigenesis is prevented in the cell.

The invention also includes a method of reversibly inducing proliferation of a cell. This method comprises providing an inhibitor of *FEZ1* expression to the interior of the cell. Proliferation of the cell is thereby induced when the inhibitor is present in the interior of the cell, but is not induced when the inhibitor is not present in the interior of the cell. The inhibitor may, for example, be an isolated polynucleotide comprising a portion which anneals with high stringency with at least twenty consecutive nucleotide residues of a strand of a human *FEZ1* gene. The isolated polynucleotide can be delivered to the interior of the cell by administering a gene vector comprising a promoter operably linked with the isolated polynucleotide to the cell. The cell can be located in the body of an animal such as a human.

In another aspect, the invention relates to a method of determining whether a test compound is an inducer of cell proliferation. This method comprises incubating a cell which comprises a functional *FEZ1* gene in the presence of the test compound and assessing expression of *FEZ1* in the cell. If expression of *FEZ1* in the cell is decreased, relative to expression of *FEZ1* in a cell of the same type incubated in the absence of the test compound, then the test compound is an inducer of cell proliferation.

The invention also includes a method of determining whether a test compound is effective to retard abnormal proliferation of a cell having an altered *FEZ1* gene. This method comprises incubating the cell in the presence of the test compound and assessing expression of *FEZ1* in the cell. If expression of *FEZ1* in the cell is increased, relative to expression of *FEZ1* in a cell of the same type incubated in the absence of the test compound, then the test compound is effective to retard abnormal proliferation of a cell.

The invention further relates to a method of determining whether Fez1 protein binds with polynucleotides having a test nucleotide sequence. This method comprises:

a) contacting Fez1 protein and a test polynucleotide having the test nucleotide sequence, and

b) thereafter assessing whether a detectably labeled Fez1-polynucleotide complex is formed. At least one of the Fez1 protein and the test polynucleotide is detectably labeled. Formation of the complex is an indication that Fez1 protein binds with polynucleotides having the test nucleotide sequence.

The invention still further relates to a method of identifying an inducer of cell proliferation. This method comprises:

a) contacting Fez1 protein and a polynucleotide with which Fez1 protein binds in the presence and absence of a test compound, and

b) assessing formation of a Fez1-polynucleotide complex. Decreased formation of the complex in the presence of the test compound, relative to formation of Fez1-polynucleotide complex in the absence of the test compound is an indication that the test compound is an inducer of cell proliferation.

The invention includes a kit for selecting an anti-cancer therapeutic compound for administration to a human afflicted with a cancer. The kit comprises a plurality of candidate anti-cancer therapeutic compounds and a reagent for assessing expression of *FEZ1* in a cell.

The invention also includes a method of inducing a cell to proliferate. This method comprises inhibiting expression of *FEZ1* in the cell. The cell is thereby induced to proliferate. In one embodiment, the cell is a cell removed from a human. This cell can thereafter be returned to the human after inhibiting expression of *FEZ1* in the cell. Alternatively, the cell can be a cell present in the body of a human. For example, expression of *FEZ1* in the cell can be inhibited by providing to the interior of the cell an isolated polynucleotide comprising a portion which anneals with high stringency with at least twenty consecutive nucleotide residues of a strand of a human *FEZ1* gene.

The invention further includes an enhanced human cell culture technique. This technique comprises incubating human cells according to a known human cell culture technique and inhibiting *FEZ1* expression in the cells.

The invention still further includes a method of detecting *FEZ1* expression in a sample tissue. This method comprises:

a) labeling an isolated antibody which binds specifically with human Fez1 protein and contacting a preparation of the isolated antibody with the sample tissue,

b) thereafter rinsing the tissue sample, whereby non-specifically bound antibodies are rinsed from the tissue sample, and

c) assessing the presence of labeled antibodies in the tissue sample. The presence of labeled antibodies in the tissue sample is an indication that *FEZ1* is expressed in the tissue sample.

The invention includes a method of determining whether a test compound is useful for alleviating a disorder associated with aberrant tubulin polymerization. The method comprises comparing

(i) tubulin polymerization in a first assay mixture which comprises tubulin, Fez1, and the test compound and

(ii) tubulin polymerization in a second assay mixture which comprises tubulin and Fez1, but which does not comprise the test compound.

A difference between (e.g. the rate or extent of) tubulin polymerization in the first and second assay mixtures is an indication that the test compound is useful for alleviating the disorder. Preferably, the first and second assay mixtures are substantially identical, but for the presence or absence of the test compound. The disorder can, for example, be a tubulin hyperpolymerization disorder or a tubulin hypopolymerization disorder, such as one of a disorder associated with aberrant initiation of mitosis, a disorder associated with aberrant modulation of the rate and stage of mitosis, a disorder associated with aberrant modulation of the initiation and rate of cell proliferation, a disorder associated with aberrant modulation of the initiation and rate of cell growth, a disorder associated with aberrant modulation of cell shape, a disorder associated with aberrant modulation of cell rigidity, a disorder associated with aberrant modulation of cell motility, a disorder associated with aberrant modulation of the rate of cellular DNA replication, a disorder associated with aberrant modulation of the stage of cellular DNA replication, a disorder associated with aberrant modulation of the intracellular distribution of organelles, a disorder associated with aberrant modulating the metastatic potential of a cell, and a disorder associated with aberrant modulation of cellular transformation from a non-cancerous to a cancerous phenotype. For example, the disorder can be one of tumorigenesis, tumor survival, tumor growth, and tumor metastasis. Examples of test compounds include a fragment of Fez1, a peptidomimetic of a fragment of Fez1, a fragment of tubulin, a peptidomimetic of a fragment of tubulin, a fragment of EF1-γ, and a peptidomimetic of a fragment of EF1-γ.

The invention also includes a method of determining whether a test compound is useful for alleviating a disorder associated with aberrant phosphorylation of Fez1. This method comprises comparing

(i) phosphorylation of Fez1 in a first assay mixture which comprises Fez1, at least one kinase, a phosphate source, and the test compound and

(ii) phosphorylation of Fez1 in a second assay mixture which comprises Fez1, the kinase, and the phosphate source, but which does not comprise the test compound.

A difference between phosphorylation of Fez1 in the first and second assay mixtures is an indication that the test compound is useful for alleviating the disorder. As with the method described in the preceding paragraph, the disorder can be one selected from the group consisting of tumorigenesis, tumor survival, tumor growth, and tumor metastasis.

The invention includes a method of determining whether a test compound is useful for alleviating a disorder associated with aberrant phosphorylation of Fez1. This method comprises comparing

(i) phosphorylation of Fez1 in a first assay mixture which comprises phosphorylated Fez1, at least one phosphatase, and the test compound and

(ii) phosphorylation of Fez1 in a second assay mixture which comprises phosphorylated Fez1 and the phosphatase, but which does not comprise the test compound.

A difference between phosphorylation of Fez1 in the first and second assay mixtures (e.g. a difference in the rate or extent of de-phosphorylation of phosphorylated Fez1) is an indication that the test compound is useful for alleviating the disorder.

In addition, the invention includes a method of determining whether a test compound is useful for alleviating a disorder associated with aberrant binding of Fez1 with a protein with which Fez1 normally binds. This method comprises comparing

(i) binding between Fez1 and the protein in a first assay mixture which comprises Fez1, the protein, and the test compound and

(ii) binding between Fez1 and the protein in a second assay mixture which comprises Fez1 and the protein, but which does not comprise the test compound,

A difference between (e.g. the rate or extent of) binding of Fez1 and the protein in the first and second assay mixtures is an indication that the test compound is useful for alleviating the disorder. Examples of the protein of this method include tubulin and EF1-γ. The disorder can, for example, be any of those recited above.

The invention further includes a method of determining whether a test compound is an inhibitor of cell proliferation. This method comprises incubating a cell

which comprises a functional *FEZ1* gene in the presence of the test compound and assessing expression of *FEZ1* in the cell. If expression of *FEZ1* in the cell is increased, relative to expression of *FEZ1* in a cell of the same type incubated in the absence of the test compound, then the test compound is an inhibitor of cell proliferation.

The invention still further includes a method of inhibiting tumorigenesis in a human, the method comprising administering to the human a compound selected from the group consisting of an inducer of *FEZ1* gene expression, an enhancer of *FEZ1* gene expression, a inhibitor of Fez1 phosphorylation, an enhancer of phosphorylated-Fez1 dephosphorylation, an agent that inhibits binding of Fez1 with EF1-γ, and an agent that inhibits binding of Fez1 with tubulin.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 comprises Figures 1A, 1B, and 1C, and each of these figures relates to loss of heterozygosity (LOH) at human chromosome 8p in primary esophageal cancer tissue samples.

Figure 1A, comprising Figures 1Ai-1Aviii, is a series of representative LOH analysis results obtained using tissue samples obtained from two patients, designated E26 and E46. Figures 1Ai, 1Aiii, 1Av, and 1Avii depict results from tissue obtained from patient E26. Figures 1Aii, 1Aiv, 1Avi, and 1Aviii depict results from tissue obtained from patient E46. In each figure, fluorescent PCR products were generated by amplification of DNA obtained from normal (N) and tumor (T) tissue samples from the corresponding patient, and products were separated by size. For each tracing, the horizontal axis represents DNA fragment size, and the vertical axis (i.e. peak height) represents relative amount of each fragment. Several fragment sizes (in base pairs) are indicated.

Figure 1B is a diagram which depicts a summary of LOH analyses described herein. Results for each patient who exhibited LOH at least at one locus are shown. Filled circles represent loss of an allele. Circles containing a cross represent non-informative results owing to homozygosity at the corresponding locus. Open

circles represent retention of both alleles. Dark shaded areas of the diagram represent regions of allele loss. Light shaded areas represent regions of non-informative results within the allele-loss area. The numbers atop each column refer to individual patients. The designations beside each row refer to polymorphic markers. The region near the marker *D8S261* locus, described herein, is boxed.

Figure 1C is a diagram which depicts the approximate locations of genomic contigs at 8p22 which were constructed as described herein. The uppermost line depicts the location of polymorphic loci on 8p. The corresponding locations of YAC contigs (open boxes) and BAC contigs (horizontal lines) are indicated below the 8p map. cDNA selection and shotgun sequencing were performed on YACs and BACs identified by asterisks. Eighty-seven potentially expressed sequences were isolated and located within the contigs; the approximate locations of these sequences are indicated by designations below two-headed arrows. Underlined characters indicate sequences which are expressed in normal tissues. After expression analysis in tumor and normal tissues, 9 cDNAs (circled designations) were subjected to further analysis. Candidate fragment e37 corresponds to the *F37* cDNA described herein.

Figure 2 comprises Figures 2A, 2B, 2C, and 2D. The predicted Fez1 amino acid sequence (SEQ ID NO: 4) is depicted in Figure 2A. Figure 2A lists the predicted amino acid sequence of FEZ1 protein, as derived from the *FEZ1* cDNA. Underlined amino acid residues represent a region homologous to the DNA-binding domain of ATF-5 protein. Double-underlined amino acid residues represent a leucine zipper motif, in which repeated leucine residues are shaded. Heavily-underlined amino acid residues are residues which can be phosphorylated by either a cAMP/cGMP-dependent kinase (serine residue 29) or a tyrosine kinase-dependent kinase (tyrosine residue 67). Dashed-underlined regions represent regions having related amino acid sequence motifs. Serine and threonine residues in bold or thin dotted lines represent potential casein kinase II and protein kinase C, respectively, phosphorylation sites. Triangles indicate exon boundaries. Asterisks represent missense or nonsense mutation sites.

In Figure 2B, the predicted amino acid sequence of a region (amino acid residues 301-369; SEQ ID NO: 6) of Fez1 corresponding to the predicted DNA binding and leucine zipper regions is compared with the analogous regions (SEQ ID NOs: 7 and 8, respectively) of proteins Atf-5 and KIAA0522. Identical amino acid residues are indicated by dark shading, and similar amino acid residues are indicated by light shading. Gaps introduced by the FASTA program are represented by "-". Closed circles are used to indicate repeated leucine residues.

Figure 2C is an image of SDS-PAGE results as described elsewhere herein.

Figure 2D is an image of Northern blot analysis results which indicate *FEZ1* gene expression in normal tissues. In the upper panel, a *FEZ1* ORF probe (SEQ ID NO: 3) was used to detect expression of *FEZ1*. In the lower panel, a beta-actin probe was used, as a control, to detect expression of the beta-actin gene. The arrowhead on the left of the top panel indicates the approximate position of the 6.8 kilobase *FEZ1* transcript. Poly(A)$^+$ RNAs (5 micrograms) were obtained from normal (i.e. non-cancerous) tissues, and loaded as follows: lane 1, heart; lane 2, brain; lane 3, placenta; lane 4, lung; lane 5, liver; lane 6, skeletal muscle; lane 7, kidney; lane 8, pancreas; lane 9, spleen; lane 10, thymus; lane 11, prostate; lane 12, testes; lane 13, ovary; lane 14, small intestine; lane 15, colon; and lane 16, peripheral blood lymphocyte.

Figure 3 comprises Figures 3A, 3B, and 3C, and relates to alterations of the *FEZ1* gene in tumor cells.

Figure 3A is an image which depicts results of Northern blot analysis of *FEZ1* gene expression in cancer cells. A *FEZ1* cDNA probe (upper panel) and a beta-actin probe (lower panel) were used to detect expression of the corresponding genes. The arrowhead on the left side of the upper panel indicates the approximate position of the 6.8-kilobase transcript of *FEZ1*. Poly(A)$^+$ RNAs (5 micrograms) were obtained from tumor cell lines, and loaded as follows: esophageal cancer cell lines KYSE170 (lane 1), TE12 (lane 2), TE8 (lane 3) and TE3 (lane 4); prostate cancer cell

lines DU145 (lane 5), LNCaP (lane 6), PC3 (lane 7); normal prostate (lane 8); breast cancer cell lines MB231 (lane 9), SKBr3 (lane 10), BT549 (lane 11), HBL100 (lane 12), MB436S (lane 13), BT20 (lane 14), MB543 (lane 15), MB175 (lane 16), MCF7 (lane 17) and T47B (lane 18); normal breast (lane 19); total RNA of normal breast (lane 20); cervical cancer cell line HeLa S3 (lane 22); chronic myelogenous leukemia cell line K562 (lane 23); lymphoblastic leukemia cell line MOLT4 (lane 24); Burkitt's lymphoma cell line Raji (lane 25); colorectal adenocarcinoma cell line SW480 (lane 26); lung cancer cell line A549 (lane 27); and melanoma cell line G361 (lane 28). Total RNA (5 micrograms) was obtained from promyelocytic leukemia cell line HL60 and loaded on lane 21.

Figure 3B, comprising Figures 3Bi-3Bvi, is a series of sequence chromatograms of *FEZ1* genes obtained from three individuals having mutated *FEZ1* genes. As indicated in Figure 3Bii, a point mutation in *FEZ1* (TCC/Ser → CCC/Pro) at codon 29 was identified in an primary esophageal cancer tissue sample obtained from patient E44. Nucleotide sequences from normal DNA from patient E44 (N) and from a BAC contig (B) are shown for comparison. A bold line overlies the altered codon. In a primary esophageal cancer tissue sample obtained from patient E50, a point mutation in *FEZ1* (AAG/Lys → GAG/Glu) was detected at codon 119 was found, as indicated in Figure 3Biv. The normal BAC sequence chromatogram is shown in Figure 3Biii. A third point mutation in *FEZ1* (CAG/Gln → TAG/STOP) at codon 501 was identified in prostate cancer cell line PC3, as indicated in Figure 3Bvi, in which the sequence chromatogram 3'- to 5'- direction. Repeated sequencing indicated the presence of a weak signal corresponding to guanine (G) within a large adenine (A) signal in the first nucleotide at codon 501, suggesting that a fraction of the cancer cells retained the normal *FEZ1* allele.

Figure 3C is an image which depicts Southern blot analysis results using the *FEZ1* gene locus. High-molecular weight DNAs from cancer cells were cleaved using restriction endonuclease *EcoR*I, separated electrophoretically, transferred to nylon membrane, and probed with the 1.7 kilobase *FEZ1* ORF probe (SEQ ID NO: 3).

The DNAs applied to each lane (10 micrograms per lane) were obtained from the following cells: lane 1, cell line MB436S; lane 2, normal placental cells obtained from a first healthy individual.; lane 3, cell line MB231; lane 4, cell line MB361; lane 5, cell line TE8; and lane 6, cell line TE3. The DNA applied to lane 7 was isolated from normal placental cells obtained from a second healthy individual.

Figure 4 comprises Figures 4A and 4B. Figure 4A is a diagram which depicts truncated *FEZ1* transcripts observed in cancer cells, as described herein. The normal exon/intron structure is indicated on the top line of the diagram, and was determined by sequencing of normal (i.e. non-cancerous) brain, prostate and esophagus cDNAs and by sequencing *FEZ1* gene in BAC. Boxes represent exons; the shaded areas represent the open reading frame (1788 base pairs; SEQ ID NO: 3). Horizontal lines represent introns, and closed circles represent point mutations which were observed, as described herein. The boxed notation "LZ" represents the approximate location of the leucine-zipper motif described herein. "FS" represents the approximate position of a frame-shift described herein. Aberrant transcripts observed in tumors are depicted by bold lines on the lines below the top line in the diagram.

Figure 4B is the putative amino acid sequence (SEQ ID NO: 6) encoded by the frame-shifted *FEZ1* transcript having a molecular weight of about 8.6 kilodaltons. Amino acid residues encoded by the frame-shifted portion of the transcript are underlined.

Figure 5, comprising Figures 5A-5P, is a series of nucleotide and amino acid sequences. Figure 5A comprises Figures 5Ai-5Aiv, and lists the nucleotide sequence (SEQ ID NO: 1) of a portion of the human genome comprising the *FEZ1* gene. Figure 5B comprises Figures 5Bi-5Biii, and lists the nucleotide sequence (SEQ ID NO: 2) of a cDNA which reflects the nucleotide sequence of the full-length mRNA transcript of wild type *FEZ1*. Figure 5C lists the nucleotide sequence (SEQ ID NO: 9) of a cDNA which reflects the nucleotide sequence of the ORF region of a truncated (E16T8) *FEZ1* mRNA transcribed by tumors cells. Figure 5D lists the nucleotide sequence (SEQ ID NO: 10) of a cDNA which reflects the nucleotide sequence of the

ORF region of a truncated (E264162) *FEZ1* mRNA transcribed by tumors cells. Figure 5E comprises Figures 5Ei and 5Eii, and lists the nucleotide sequence (SEQ ID NO: 11) of a cDNA which reflects the nucleotide sequence of the ORF region of a truncated (T8D145M4) *FEZ1* mRNA transcribed by tumors cells. Figure 5F lists the nucleotide sequence (SEQ ID NO: 12) of a cDNA which reflects the nucleotide sequence of the ORF region of a truncated (D14) *FEZ1* mRNA transcribed by tumors cells. Figure 5G lists the nucleotide sequence (SEQ ID NO: 13) of a cDNA which reflects the nucleotide sequence of the ORF region of a truncated (G3611) *FEZ1* mRNA transcribed by tumors cells. Figure 5H comprises Figures 5Hi and 5Hii, and lists the nucleotide sequence (SEQ ID NO: 14) of a cDNA which reflects the nucleotide sequence of the ORF region of a truncated (G3612) *FEZ1* mRNA transcribed by tumors cells. Figure 5I lists the nucleotide sequence (SEQ ID NO: 3) of a cDNA which reflects the nucleotide sequence of the ORF region of wild type *FEZ1* mRNA. Figure 5J lists the amino acid sequence (SEQ ID NO: 4) of full-length, human wild type Fez1 protein. Figure 5K lists the amino acid sequence (SEQ ID NO: 15) of a truncated (E16T8) Fez1 protein expressed by tumors cells. Figure 5L lists the amino acid sequence (SEQ ID NO: 16) of a truncated (E264162) Fez1 protein expressed by tumors cells. Figure 5M lists the amino acid sequence (SEQ ID NO: 17) of a truncated (T8D145M4) Fez1 protein expressed by tumors cells. Figure 5N lists the amino acid sequence (SEQ ID NO: 18) of a truncated (D14) Fez1 protein expressed by tumors cells. Figure 5O lists the amino acid sequence (SEQ ID NO: 19) of a truncated (G3611) Fez1 protein expressed by tumors cells. Figure 5P lists the amino acid sequence (SEQ ID NO: 20) of a truncated (G3612) Fez1 protein expressed by tumors cells. Figure 5Q lists the nucleotide sequence (SEQ ID NO: 21) of the *F37* probe described herein.

Figure 6 is an image of an immunoblot of proteins isolated from MCF7 cell line clones which had been transfected with pTet-Off™ vector alone ("control") or with the vector having at least the coding portion of the *FEZ1* gene operably linked with the promoter thereof (clones 118, 54, 18, and 15). Proteins were isolated from cells which had been maintained in the presence ("+") or absence ("-") of tetracycline.

Figure 7, comprising Figures 7A, 7B, 7C, and 7D, is a quartet of graphs which indicate the time dependence of the ratio of transfected MCF7 clone cell number to control cell number for cells maintained in tetracycline-free medium containing 10% (○), 5% (●), 2.5% (□), 1% (■), or 0.5% (▲) (v/v) fetal bovine serum.

Figure 8 , comprising Figures 8A and 8B, is a pair of graphs which indicate the ratios of the number of transfected MCF7 clone cells which were in the G2 cell cycle stage, relative to the number in the M stage (Figure 8A; i.e., G2/M) or the ratio of the number of cells in the S phase, relative to the number in the G1 stage (Figure 8B; i.e., S/G1). In these figures, solid lines correspond to clone 18, and broken lines correspond to clone 54. Filled circles correspond to ratios in the of presence tetracycline (i.e. non-expression of *FEZ1*), and open circles correspond to ratios in the absence of tetracycline (i.e. expression of *FEZ1*).

Figure 9, comprising Figures 9A and 9B, is a pair of graphs which indicate the temporal dependence of tumor volume in nude mice into which about 5×10^6 (Figure 9A) or about 2×10^7 (Figure 9B) MCF7 cells transfected with vector alone (○), transfected MCF7 clone 15 cells (●), transfected MCF7 clone 18 cells (■), transfected MCF7 clone 56 cells (□), or transfected MCF7 clone 118 cells (◊) were implanted.

Figure 10, comprising Figures 10A-10F, lists the nucleotide sequence (SEQ ID NO: 60) of pQBI-AdCMV5-IRES-GFP.

Figure 11, comprising Figures 11A, 11B, and 11C, is a trio of images of the results of an *in vitro* binding assay demonstrating binding between ^{35}S-methionine-labeled EF1-γ and Fez1 protein.

Figure 12 is an image of the results of an *in vitro* binding assay demonstrating binding between ^{35}S-methionine-labeled EF1-γ(N) and Fez1 protein and between EF1-γ(N) and a truncated Fez1 protein.

Figure 13 is an image of the results of an *in vitro* binding assay demonstrating dimerization of Fez1 protein and dimerization of truncated Fez1 protein.

Figure 14 is a series of four images which depict the results of immunoblotting experiments involving HeLaS3 cells which were co-transfected with a vector encoding a V5/Fezl fusion protein and a vector encoding an EXP/EF1-γ fusion protein.

Figure 15, comprising Figures 15A and 15B, is a pair of images of the results of immunoblotting experiments.

Figure 16, comprising Figures 16A and 16B, is a pair of images of the results of immunoblotting experiments in synchronized, transfected MCF7 cells, using an antibody which binds specifically with Fezl ("Fezl") and an antibody which binds specifically with actin ("actin"). Numbers above the columns indicate the elapsed time following aphidicolin treatment. The proteins immunoblotted in the experiments corresponding to Figure 16A were obtained from transfected MCF7 cells which were maintained in the presence of 10% (v/v) FBS, and the proteins immunoblotted in the experiments corresponding to Figure 16B were obtained from transfected MCF7 cells which were maintained in the absence of FBS.

Figure 17 is an image of the results of an immunoblotting experiment involving proteins extracted from cell cycle-synchronized fetal kidney 293 cells.

Figure 18 is an image of the results of an SDS-PAGE separation of the proteins obtained from the cells corresponding to Figure 16A. The cells corresponding to lanes 1, 2, 3, and 4 in Figure 18 correspond to lanes designated 0, 1.5, 5, and 9 in Figure 16A.

Figure 19 is an image of the results of an immunoblotting experiment in which the cell lysates used in the experiments corresponding to Figure 16A were contacted with alkaline phosphatase (lane 1), β-glycerophosphate (lane 2), or a control.

Figure 20 is an image of SDS-PAGE separated Fezl proteins obtained from synchronized, transfected MCF7 cells and immunoblotted with either an anti-Fezl polyclonal antibody (lanes 6-10) or an anti-phosphoserine antibody (lanes 1-5) at increasing times from 0 (lanes 1 and 6) to 8 hours (lanes 5 and 10) following cessation of cell cycle inhibition.

Figure 21 is an image of the results of an experiment in which cytoplasmic ("C1" and "C2") and nuclear ("N") protein extracts obtained from 293 cells were immunoblotted using a polyclonal anti-Fez1 antibody ("Fez1") or an anti-tubulin antibody ("tubulin").

Figure 22 is an image of the results of an experiment in which Fez1 protein which Fez1 protein "Fez1" was detected using a polyclonal antibody in extracts obtained from centrifugation-sedimented cell structures in synchronized cells which had been incubated with paclitaxel ("Tax") or with colchicine ("Col").

Figure 23 is a graph which indicates the effect of Fez1 protein on inhibition of tubulin polymerization in the presence of MAP2 protein. Reaction mixtures contained, in addition to reaction buffer: nothing (open circle); tubulin (open diamond); tubulin and MAP2 (open square); tubulin, MAP2, and GST (diamond enclosing cross); tubulin, MAP2, and GST-fused Fez1 (filled circle); tubulin, MAP2, GST-fused mutated (29 Ser Pro) Fez1 (filled square); tubulin, MAP2, and PKA-phosphorylated GST-fused Fez1 (circle enclosing cross); and tubulin, MAP2, and PKA-phosphorylated GST-fused mutated (29 Ser Pro) Fez1 (square enclosing cross). "PKA" is protein kinase A, a 3':5'-monophosphate-dependent protein kinase.

DETAILED DESCRIPTION

The present invention is based on the discovery, isolation, and sequencing of *FEZ1*, a tumor suppressor gene located at human chromosome location 8p22. It was observed that decreased, or no, expression of *FEZ1* could be detected in a variety of cancer cells obtained from cancer cell lines and cancer tissue samples taken from human patients. Cancer types in which abnormal (i.e. decreased or no) expression of *FEZ1* has been detected include, but are not limited to, epithelial cancers, cancers of the digestive system, esophageal cancers, gastric cancers, colon cancers, prostate cancers, breast cancers, hematopoietic cancers, lung cancers, melanomas, and cervical

cancers, as described herein. It is contemplated that expression of *FEZ1* will be implicated in other cancers, once those cancers are tested for altered *FEZ1* expression.

Expression of *FEZ1* inhibits tumor growth and proliferation, both *in vitro* and *in vivo*. The ability of Fez1 protein to interact with tubulin, with microtubules, and with protein EF1-γ indicates that expression of *FEZ1* in cells modulates microtubule-associated physiological processes such as mitosis, cell proliferation, cell motility, and the like. Furthermore, post-translational phosphorylation and de-phosphorylation of Fez1 protein can modulate the effect that Fez1 protein has on these physiological processes.

Definitions

As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (i.e. to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

The terms "cancerous" (e.g., cell, tissue, state, etc.) and "tumor" (cell, tissue, state, etc.) are used interchangeably herein.

A "polynucleotide" means a single strand or parallel and anti-parallel strands of a nucleic acid. Thus, a polynucleotide can be either a single-stranded or a double-stranded nucleic acid.

An "isolated" polynucleotide is one which refers to a nucleic acid segment or fragment which is separated from sequences which flank it in a naturally occurring state, *e.g.*, a DNA fragment which is not adjacent to the sequences which are normally adjacent to the fragment, *e.g.*, the sequences adjacent to the fragment in a genome in which it naturally occurs. The term also applies to nucleic acids which are substantially purified from other components which naturally accompany the nucleic acid, *e.g.*, RNA or DNA or proteins, which naturally accompany it in the cell. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of

a prokaryote or eukaryote, or which exists as a separate molecule (e.g., as a cDNA or a genomic or cDNA fragment produced by PCR or restriction enzyme digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

An "isolated" protein or antibody is one which is separate from one or more other components which naturally accompany it in its naturally occurring state. By way of example, an isolated protein can be prepared by separating a protein from at least one other protein which naturally accompanies it. Further by way of example, an isolated protein can be prepared by synthesizing the protein in the absence of at least one other protein which naturally accompanies it.

A "substantially purified" polynucleotide, protein, or antibody is one which is separate from at least most of the components which naturally accompany it in its naturally occurring state, and preferably from at least 75%, 80%, 90%, or even 95% of those components, as assessed on a per-weight basis or a per-mole basis.

"Homologous" as used herein, refers to the subunit sequence similarity between two polymeric molecules, *e.g.*, between two nucleic acid molecules, *e.g.*, two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit, *e.g.*, if a position in each of two DNA molecules is occupied by adenine, then they are homologous at that position. The homology between two sequences is a direct function of the number of matching or homologous positions, *e.g.*, if half (*e.g.*, five positions in a polymer ten subunits in length) of the positions in two compound sequences are homologous then the two sequences are 50% homologous, if 90% of the positions, *e.g.*, 9 of 10, are matched or homologous, the two sequences share 90% homology. By way of example, DNA sequences 3'-ATTGCC-5' and 3'-TATGGC-5' share 50% homology.

"Substantially homologous" means having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or even at least 99% homology.

"Completely homologous" means having 100% homology.

"Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is anti-parallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is anti-parallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an anti-parallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an anti-parallel fashion, at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion, in which event, the two portions are described as being "completely complementary." "Substantially complementary" means having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or even at least 99% complementarity.

A first polynucleotide "anneals" with a second polynucleotide if the nucleotide residues of at least one region of each of the two polynucleotides participate in base pairing when the two regions are arranged in an anti-parallel fashion in an appropriate solution. Such solutions are well known in the art and include, e.g. standard saline citrate (SSC) buffer.

A first polynucleotide anneals "with high stringency" with a second polynucleotide if the two polynucleotides anneal under conditions whereby only oligonucleotides which are at least about 75%, and preferably at least about 90% or at least about 95%, complementary anneal with one another. The stringency of

conditions used to anneal two polynucleotides is a function of, among other factors, temperature, ionic strength of the annealing medium, the incubation period, the length of the polynucleotides, the G-C content of the polynucleotides, and the expected degree of non-homology between the two polynucleotides, if known. Methods of adjusting the stringency of annealing conditions are known (see, e.g. Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York). By way of example, high stringency hybridization conditions include hybridizing conditions that (1) employ low ionic strength and high temperature for washing, for example, 0.015 molar NaCl, 1.5 millimolar sodium citrate, and 0.1% (w/v) sodium dodecyl sulfate (SDS) at 50°C; (2) employ during hybridization a denaturing agent such as formamide, for example, 50% (v/v) formamide, 0.1% (w/v) bovine serum albumin, 0.1% (w/v) Ficoll, 0.1% (w/v) polyvinylpyrrolidone, and 50 millimolar sodium phosphate buffer at pH 6.5 with 750 millimolar NaCl, 75 millimolar sodium citrate at 42°C; or (3) employ 50% (v/v) formamide, 5 × SSC (0.75 molar NaCl, 75 millimolar sodium pyrophosphate, 5 × Denhardt's solution, sonicated salmon sperm DNA (50 micrograms per milliliter), 0.1% (w/v) SDS, and 10% (w/v) dextran sulfate at 42°C, with washes at 42°C in 0.2 × SSC and 0.1% (w/v) SDS. Under stringent hybridization conditions, only highly complementary nucleic acids hybridize.

A "functional" or "operative" protein is a protein in a form which exhibits at least one biological activity by which it is characterized in its naturally occurring state.

A "functional" or "operative" gene is a gene which, when present in an environment comprising functional gene expression proteins (e.g. the interior of a human cell or an *in vitro* gene expression mixture of a type described in the art), is expressed to yield the gene product encoded or specified by the gene.

A first polynucleotide is "specified" by a second polynucleotide if the first polynucleotide is either homologous with or complementary to a transcript polynucleotide generated either by transcription or by reverse transcription of at least a portion of the second polynucleotide. The first polynucleotide can be homologous with

or complementary to the transcript polynucleotide either before or after the transcript polynucleotide has been acted upon by eukaryotic mRNA splicing components.

A "portion" or "region" of a polynucleotide means at least two consecutive nucleotide residues of the polynucleotide, and preferably at least 10, 11, 12, ..., 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 or more consecutive nucleotide residues.

A first portion of a polynucleotide is "adjacent" a second portion of the same polynucleotide if the nucleotide sequences of the first and second portions are directly attached to one another, having no intervening nucleotides. By way of example, the pentanucleotide 5'-AAAAA-3' is adjacent the trinucleotide 5'-TTT-3' when the two are connected thus: 5'-AAAAATTT-3' or 5'-TTTAAAAA-3', but not when the two are connected thus: 5'-AAAAACTTT-3'.

A first portion of a polynucleotide "flanks" a second portion of the same polynucleotide if the two portions are adjacent one another or if the two portions are separated by no more than about 1000, 999, 998, ..., 900, 899, 898, ..., 750, 749, 748, ..., 500, 499, 498, ..., 250, 249, 248, ..., and preferably no more than about 100 nucleotide residues.

SUB B1 D> By describing two polynucleotides as "operably linked" is meant that a single-stranded or double-stranded nucleic acid moiety comprises the two polynucleotides arranged within the nucleic acid moiety in such a manner that at least one of the two polynucleotides is able to exert a physiological effect by which it is characterized upon the other. By way of example, a promoter operably linked with the coding region of a gene is able to promote transcription of the coding region.

As used herein, the term "promoter " means a nucleic acid sequence which is required for expression of a gene product operably linked with the promoter sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The

promoter sequence may, for example, be one which expresses the gene product in a tissue specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

The "substantial absence of expression" of a gene means that the level of expression of the gene is undetectable or is at least greatly reduced (e.g. 100-fold or 1000-fold or more) relative to expression of the gene in its naturally occurring state.

An "expression vector" is a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell, such that a gene product encoded by or specified by the isolated nucleic acid is generated in the cell. Numerous expression vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Expression vectors generally either comprise a promoter operably linked with a portion of the isolated nucleic acid which encodes or specifies a gene product, or are capable of inserting the isolated nucleic acid into a cellular nucleic acid wherein the portion is operably linked with a cellular promoter.

An "exogenous" polynucleotide in an organism is one which is not present in a naturally-occurring form of the organism in the same form as the

polynucleotide. By way of example, an exogenous polynucleotide can be one which comprises a nucleotide sequence which the genome of the organism does not comprise, or it can be one which comprises a portion of the organism's genome in a form (e.g. a plasmid or an artificial chromosome) which is not present in a naturally-occurring form of the organism.

An "analog" of a gene is one is substantially homologous with the gene and which encodes or specifies a gene product having a biological activity which is substantially the same as a biological activity exhibited by the gene product encoded or specified by the gene.

A "*FEZ1*-associated polynucleotide" means a polynucleotide which comprises a portion which is substantially homologous with or substantially complementary to at least about 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 or more consecutive nucleotide residues of either a human *FEZ1* gene or a spliced mRNA specified by a human *FEZ1* gene.

A "*FEZ1*-transcript-associated polynucleotide" means a polynucleotide which comprises a portion which is substantially homologous with or substantially complementary to at least about 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 or more consecutive nucleotide residues of either a spliced or non-spliced mRNA specified by a human *FEZ1* gene.

"Contigs" of a genomic region are a collection of oligonucleotides, usually contained in a yeast, bacterial, or phage vector, which together include all or substantially all (i.e. >95%, and preferably >99%) of the sequence of the genomic region.

An "exon boundary polynucleotide probe" is a polynucleotide which is complementary to or homologous with at least five nucleotide residues of an exon of a *FEZ1* gene which are adjacent to an intron of that gene.

A "protein-ligand pair" refers to a protein and another molecule, wherein the protein specifically binds with the other molecule. Examples of protein-

ligand pairs include an antibody and its corresponding epitope and an avidin protein, such as streptavidin, and biotin.

A protein or polynucleotide is "detectably labeled" if the protein or polynucleotide comprises or is linked with a composition of matter which can be detected after contacting the protein or polynucleotide with another protein or polynucleotide. Innumerable methods are known in the art for detectable labeling proteins and polynucleotides including, for example, surfaces with which such compounds are linked, radionuclides incorporated into such proteins, chromophores and fluorophores which are linked with such compounds, and the like.

A "gene chip" is a manufacture comprising a surface having an ordered array of polynucleotides attached thereto, either permanently or reversibly. For example, the ordered array can comprise four sections, wherein one of four polynucleotides is attached to the surface in each section, and wherein the four polynucleotides have nucleotides sequences which are identical with the exception of one nucleotide residue (e.g. 5'-AACCAAAAAAA-3'; 5'-AACCAAAAAAT-3'; 5'-AACCAAAAAAC-3'; and 5'-AACCAAAAAAG-3').

An "inducer of cell proliferation" is a composition of matter which, when contacted with a cell, causes the cell to grow, divide, or replicate at a rate greater than the corresponding rate in the absence of the composition.

Cell proliferation is "retarded" if the rate of cell proliferation is reduced.

The "cancerous state" of a tissue or cell refers to whether the cell or one or more cells within the tissue have accumulated enough genomic mutations that they either presently exhibit one or more characteristics of tumor cells or tissue (e.g. uncontrolled cell proliferation or metastasis) or, will, without further genomic damage, exhibit one or more characteristics of tumor cells or tissue upon incubation or maintenance of the cell.

A "phenotypically abnormal" portion of a tissue is one which comprises cells which have one or more characteristics of cancer cells of the tissue type such as, for example, abnormal morphology or abnormal growth or proliferation rate.

A "phenotypically normal" portion of a tissue is one which does not appear to be phenotypically abnormal.

A "candidate anticancer compound" is a compound which has exhibited potential anti-cancer activity in a relevant assay or a compound which has substantial structural similarity to such a compound. Methods of identifying a compound which exhibits potential anti-cancer activity and methods of designing structurally similar compounds are well known in the art.

The term "pharmaceutically acceptable carrier" means a chemical composition with which one or more active ingredients can be combined and which, following the combination, can be used to administer one or more active ingredients to a subject.

The term "physiologically acceptable" ester or salt means an ester or salt form of an active ingredient which is compatible with any other ingredients of the pharmaceutical composition and which is not deleterious to the subject to which the composition is to be administered.

An "instructional material" means a publication, a recording, a diagram, or any other medium of expression which can be used to communicate the usefulness of an isolated polynucleotide, an isolated protein, or a pharmaceutical composition of the invention for performing one or more of the methods of the invention. The instructional material may, for example, describe how to use one of these compositions to perform a diagnostic method of the invention, a therapeutic method of the invention, or a screening assay of the invention, or, for example, an appropriate dose of a pharmaceutical composition of the invention.

A "tubulin hyperpolymerization disorder" is a disorder which is associated with a greater extent or rate of tubulin polymerization in a cell or animal afflicted with the disorder than in a cell or animal which is not afflicted with the disorder.

A "tubulin hypopolymerization disorder" is a disorder which is associated with a lesser extent or rate of tubulin polymerization in a cell or animal

afflicted with the disorder than in a cell or animal which is not afflicted with the disorder.

Description

Being a tumor suppressor gene, *FEZ1* is intimately involved in control of the cancerous or non-cancerous phenotype of a cell which normally expresses it. Characteristics of tumor cells which normally express *FEZ1* include abnormal cell proliferation, abnormal cell growth, and abnormal differentiation of cells.

In normal (i.e. non-cancerous) cells, expression of *FEZ1* limits cell proliferation. While not wishing to be bound by any particular theory of operation, it is thought that a leucine-zipper region described herein within the putative structure of Fez1 protein is involved in binding between Fez1 and one or more regions of a physiological polynucleotide (e.g. genomic DNA), whereby expression (i.e. transcription or translation) of the polynucleotide is inhibited or prohibited. Binding between Fez1 and one or more regions on the human genome can inhibit transcription of one or more genes located nearby on the genome, and is contemplated as a potential mechanism of action for *FEZ1* regulation of cell proliferation. Nonetheless, the possibility that Fez1 protein binds to and regulates translation of mRNA cannot be excluded. Regardless of the manner in which *FEZ1* expression or non-expression serves to regulate cell proliferation, the compositions and methods described herein are useful for the purposes described herein.

The nucleotide sequence (SEQ ID NO: 1) of a portion of the human genome encoding wild type *FEZ1* is shown in Figure 5A. The nucleotide sequence (SEQ ID NO: 2) of cDNA generated using full-length mRNA transcribed from wild type *FEZ1* is shown in Figure 5B. The nucleotide sequence (SEQ ID NO: 3) of the open reading frame (ORF) of wild type *FEZ1* is shown in Figure 5I. The putative amino acid sequence (SEQ ID NO: 4) of wild type Fez1 protein is shown in Figure 5J. Nucleotide sequences (SEQ ID NOs: 9-14) of cDNAs generated using truncated *FEZ1* mRNA species and amino acid sequences (SEQ ID NOs: 15-20) of corresponding

truncated Fez1 proteins are shown in Figures 5C to 5H and in Figures 5K to 5P, respectively.

The Isolated Polynucleotide of the Invention

The invention includes an isolated polynucleotide which anneals with high stringency with at least twenty consecutive nucleotide residues of at least one strand of the human *FEZ1* gene, such as a human gene having the sequence SEQ ID NO: 1. Preferably, the isolated polynucleotide of the invention anneals with high stringency with at least 20, 21, 22, ..., 30, 31, 32, ..., 50, 51, 52, ..., 75, 76, 77, ..., or 100 consecutive nucleotide residues of at least one strand of the human *FEZ1* gene, or is substantially complementary with those residues. In certain embodiments, it is preferred that the isolated polynucleotide of the invention have a length not greater than about 200, 199, 198, ... 150, 149, 148, ..., 100, 99, 98, ..., 50, 49, 48, ..., 40, 39, 38, ..., or 35 nucleotide residues.

The isolated polynucleotide of the invention preferably has a sequence that is substantially homologous with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 consecutive nucleotide residues of at least one strand of the human *FEZ1* gene. More preferably, the isolated polynucleotide of has a sequence completely homologous with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 consecutive nucleotide residues of at least one strand of the human *FEZ1* gene, and even more preferably with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 consecutive nucleotide residues of at least one strand of SEQ ID NO: 1.

The isolated polynucleotide of the invention can be selected to be homologous with either the coding strand or the non-coding strand of *FEZ1*. Alternately, the isolated polynucleotide can comprise both a first portion that is homologous with one strand of *FEZ1* and a second portion that is homologous with the other strand, such an isolated polynucleotide that is capable of forming a hairpin-type structure when the first portion thereof anneals with the second. Depending on the use to which the isolated polynucleotide of the invention is to be put, the skilled artisan will be able, in light of the present disclosure, to decide whether the isolated polynucleotide

should comprise a portion homologous with the coding strand of *FEZ1*, a portion homologous with the non-coding strand, or both.

It is understood that, depending on the use to which the isolated polynucleotide of the invention is to be put and the length of the isolated polynucleotide, the degree of homology between the isolated polynucleotide and the at least one strand of human *FEZ1* can be more or less critical in various embodiments described herein.

When the isolated polynucleotide of the invention is to be hybridized or annealed with a nucleic acid having a sequence wherein at least a portion is complementary to the isolated polynucleotide, the necessary degree of homology between the isolated polynucleotide and the at least one strand of *FEZ1* is dependent on the length of the polynucleotide. As is well known, as the length of a polynucleotide increases, the degree of complementarity necessary to anneal the polynucleotide with another polynucleotide with high stringency decreases. Numerous methods, algorithms, computer programs, and the like are known whereby the skilled artisan can predict the stringency of binding between two polynucleotides (e.g. Suhai, Ed., 1992, Computational Methods in Genome Research, Plenum Press, New York; Swindell, Ed., 1997, Sequence Data Analysis Guidebook, Humana Press, New Jersey; Bishop, Ed., 1998, Guide to Human Genome Computing, Academic Press, New York). Any of these methods, etc., can be used by the skilled artisan, in light of the present disclosure, to design or select isolated polynucleotides of various lengths which will anneal with at least one strand of a human *FEZ1* gene with high affinity. All such isolated polynucleotides are included within the invention.

The determination of percent identity between two nucleotide or amino acid sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et

al. (1990, J. Mol. Biol. 215:403-410), and can be accessed, for example at the National Center for Biotechnology Information (NCBI) world wide web site having the universal resource locator "http://www.ncbi.nlm.nih.gov/BLAST/". BLAST nucleotide searches can be performed with the NBLAST program (designated "blastn" at the NCBI web site), using the following parameters: gap penalty = 5; gap extension penalty = 2; mismatch penalty = 3; match reward = 1; expectation value 10.0; and word size = 11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with the XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically exact matches are counted.

When the isolated polynucleotide of the invention is to be used to express all or a portion of a human Fez1 protein, either *in vitro* or *in vivo*, it is important that (i) the homology of the isolated polynucleotide with the human *FEZ1* gene (e.g. SEQ ID NO: 1) is such that the amino acid sequence encoded by the isolated polynucleotide is identical to the corresponding region of *FEZ1*, (ii) the differences between the sequence of the isolated polynucleotide and the corresponding region of *FEZ1* not result in differences in the encoded amino acid sequence (i.e. any sequence

difference in a coding region merely substitutes a codon encoding an amino acid in place of another codon encoding the same amino acid), or (iii) any differences in the encoded amino acid sequence between the isolated polynucleotide and the corresponding region of *FEZ1* results only in one or more conservative amino acid substitutions, as described in greater detail elsewhere herein. The following Human Codon Table can be used to select or identify alternate codons which encode the same amino acid.

Human Codon Table

Amino Acid	Codons Encoding the Amino Acid
Alanine	GCA GCC GCG GCU
Cysteine	UGC UGU
Aspartic acid	GAC GAU
Glutamic acid	GAA GAG
Phenylalanine	UUC UUU
Glycine	GGA GGC GGG GGU
Histidine	CAC CAU
Isoleucine	AUA AUC AUU
Lysine	AAA AAG
Leucine	UUA UUG CUA CUC CUG CUU
Methionine	AUG
Asparagine	AAC AAU
Proline	CCA CCC CCG CCU
Glutamine	CAA CAG
Arginine	AGA AGG CGA CGC CGG CGU
Serine	AGC AGU UCA UCC UCG UCU
Threonine	ACA ACC ACG ACU
Valine	GUA GUC GUG GUU
Tryptophan	UGG
Tyrosine	UAC UAU

In situations in which it is necessary or desirable to introduce nucleotide residue changes into a polynucleotide such as the isolated polynucleotide of the invention, or into a Fez1 protein or a portion thereof, a variety of well-known techniques can be used, such as site-specific mutagenesis. Site-specific mutagenesis, for example, allows production of mutants through the use of specific oligonucleotides which encode the sequence of the desired mutation, as well as a sufficient number of

adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complementarity to form a stable duplex on both sides of the nucleotide sequence to be altered (e.g. a codon). Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered. This technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as M13 phage. Such vectors are commercially available, and their use is well known in the art. Double stranded plasmids are also routinely employed in site-directed mutagenesis protocols, to eliminate the need to transfer the gene of interest from a plasmid to a phage vector. Site-directed mutagenesis is performed by first obtaining a single-stranded vector or dissociating the two strands of a double stranded vector which includes within its sequence a DNA sequence which comprises the desired site of mutagenesis. The oligonucleotide primer described above is annealed with the single-stranded vector, and subjected to DNA polymerization, in order to generate a mutation-bearing strand. A heteroduplex is formed between the mutation-bearing strand and either the original non-mutated strand of the double-stranded vector or an added or synthesized strand which is substantially complementary to the mutation-bearing strand. This heteroduplex is then used to transform appropriate cells, such as *E. coli* or cultured human cells, and clones are selected which comprise recombinant vectors bearing the mutated sequence arrangement. Preparation of sequence variants of the isolated polynucleotide of the invention using site-directed mutagenesis is provided merely as an example of a method of producing potentially such variants, and is not intended to be limiting, as there are other well-known methods for producing such variants. By way of example, recombinant vectors comprising or encoding the desired isolated polynucleotide can be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

The isolated polynucleotide of the invention can be single stranded or double-stranded, it being understood that a single-stranded form is the form referred to

herein when annealing of the isolated polynucleotide of the invention with another nucleic acid is described.

The isolated polynucleotide of the invention can be substantially any nucleic acid, whether composed of deoxyribonucleosides or ribonucleosides, and whether composed of phosphodiester linkages or modified linkages such as phosphotriester, phosphoramidate, siloxane, carbonate, carboxymethyl ester, acetamidate, carbamate, thioether, bridged phosphoramidate, bridged methylene phosphonate, bridged phosphoramidate, bridged phosphoramidate, bridged methylene phosphonate, phosphorothioate, methylphosphonate, phosphorodithioate, bridged phosphorothioate or sulfone linkages, and combinations of such linkages. The term nucleic acid also specifically includes nucleic acids composed of bases other than the five biologically occurring bases (adenine, guanine, thymine, cytosine, and uracil). The isolated polynucleotide of the invention is preferably in a substantially purified form.

It is not intended that the present invention be limited by the nature of the nucleic acid employed. The isolated polynucleotide of the invention can be an isolated, naturally occurring nucleic acid or it can be a synthetic nucleic acid. The isolated, naturally occurring nucleic acid can obtained be from a viral, bacterial, animal, human, or plant source. The polynucleotide can be DNA or RNA. Furthermore, the nucleic acid can be isolated, synthesized, or assembled as part of a virus or other macromolecule. *See, e.g.,* Fasbender *et al.,* 1996, *J. Biol. Chem.* 272:6479-89 (polylysine condensation of DNA in the form of adenovirus).

Nucleic acids useful in the present invention include, by way of example and not limitation, oligonucleotides and polynucleotides such as antisense DNAs and/or RNAs; ribozymes; DNA for gene therapy; viral fragments including viral DNA and/or RNA; DNA and/or RNA chimeras; mRNA; plasmids; cosmids; genomic DNA; cDNA; gene fragments; various structural forms of DNA including single-stranded DNA, double stranded DNA, supercoiled DNA and/or triple-helical DNA; Z-DNA; and the like. The nucleic acids can be prepared by any conventional means typically used to prepare nucleic acids in large quantity. For example, DNAs and RNAs can be

chemically synthesized using commercially available reagents and synthesizers by methods that are well-known in the art (see, *e.g.*, Gait, 1985, Oligonucleotide Synthesis: A Practical Approach (IRL Press, Oxford, England)). RNAs can be produce in high yield via *in vitro* transcription using plasmids such as SP65 (Promega Corporation, Madison, WI).

In some circumstances, as where increased nuclease stability is desired, nucleic acids having modified internucleoside linkages can be preferred. Nucleic acids containing modified internucleoside linkages can also be synthesized using reagents and methods that are well known in the art. For example, methods for synthesizing nucleic acids containing phosphonate, phosphorothioate, phosphorodithioate, phosphoramidate methoxyethyl phosphoramidate, formacetal, thioformacetal, diisopropylsilyl, acetamidate, carbamate, dimethylene-sulfide ($-CH_2-S-CH_2$), dimethylene-sulfoxide ($-CH_2-SO-CH_2$), dimethylene-sulfone ($-CH_2-SO_2-CH_2$), 2'-O-alkyl, and 2'-deoxy-2'-fluoro phosphorothioate internucleoside linkages are well known in the art (Uhlmann et al., 1990, Chem. Rev. 90:543-584; Schneider et al., 1990, Tetrahedron Lett. 31:335). Stability of the isolated polynucleotide of the invention can also be enhanced by treating on or both ends of the polynucleotide (if it is linear) with at least one agent which nucleolytically blocks the end. Such agents are known in the art (e.g. agents described in Oligonucleotides as Therapeutic Agents, 1997, John Wiley & Sons, New York).

The isolated polynucleotide can be purified by any suitable means, such as are well known in the art. For example, the isolated polynucleotide can be purified by reverse phase or ion exchange HPLC, size exclusion chromatography, or gel electrophoresis. Of course, the skilled artisan will recognize that the method of purification will depend in part on the size and type of the nucleic acid to be purified and on the characteristics of any molecules, structure, or organisms with which it can be associated. It is furthermore contemplated that the isolated polynucleotide of the invention can comprise nucleotide residues other than the five naturally occurring bases, adenine, guanine, thymine, cytosine, and uracil.

In certain embodiments, the isolated polynucleotide of the invention is detectably labeled. Any known method of labeling a nucleic acid can be used to label the polynucleotide. By way of example, well known methods of detectably labeling a polynucleotide include incorporation of a radionuclide into the polynucleotide, linking the polynucleotide to a surface, such as a latex bead or a nylon membrane, linking a protein such as an enzyme to the polynucleotide, linking one of a protein-ligand pair (e.g. an avidin-biotin pair or an antibody-antigen pair) to the polynucleotide, linking a chromophore to the polynucleotide, and linking a fluorophore to the polynucleotide. In one embodiment useful for quantification of a nucleic acid with which the isolated polynucleotide of the invention is capable of annealing, the isolated polynucleotide is reversibly linked with both a fluorophore and a molecule capable of quenching the fluorescence of the fluorophore, whereby if either the fluorophore or the quenching molecule is dissociated from the isolated polynucleotide, then enhanced fluorescence of the fluorophore is detectable, as described (Livak et al., 1995, "Guidelines for Designing TaqMan™ Fluorogenic Probes for 5' Nuclease Assays", Perkin Elmer, Norwalk, CT; U.S. Patent No. 5,210,015; U.S. Patent No. 5691,146; Heid et al., 1996, Genome Res. 6:986-994).

The isolated polynucleotide of the invention has numerous uses. For example, such an isolated polynucleotide can be detectably labeled and used as a probe to detect the presence of a different polynucleotide having a sequence comprising a portion to which it anneals (e.g. a genome, genomic fragment, mRNA, cDNA, DNA, or library clone encoding human *FEZ1*). Such a probe can be used, for example, to detect or to quantify expression of *FEZ1* in a cell or tissue of a human. It is understood that numerous methods of using a polynucleotide probe for detection and quantification of nucleic acids with which the probe anneals are known in the art (e.g. Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York; Ausubel et al., 1992, Current Protocols in Molecular Biology, John Wiley & Sons, New York; Gerhardt et al., eds., 1994, Methods for General and Molecular Bacteriology, American Society for Microbiology, Washington, DC), and these

methods are therefore not described here in detail. When the probe is used for detection or quantification of a nucleic acid encoding all or a portion of *FEZ1*, it is preferably detectably labeled.

The isolated polynucleotide of the invention can similarly be used to detect the presence of a non-human analog of the human *FEZ1* gene in a polynucleotide obtained or derived from a non-human source (e.g. a library of genomic fragments obtained from, or a library of cDNAs derived from mRNAs of, an animal such as a mammal). It is well known that gene sequences are conserved among animals, the degree of sequence conservation being generally associated with the degree of evolutionary relatedness of the animals. Thus, it is contemplated that isolated polynucleotides which anneal with high stringency with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 consecutive nucleotide residues of human *FEZ1*, or which are substantially complementary with those residues, are useful for identifying genomic fragments, cDNAs, mRNAs, or other polynucleotides which comprise a portion of an animal *FEZ1* gene which is analogous to the portion of the human *FEZ1* gene with which the isolated polynucleotide of the invention anneals. Given the fact that human *FEZ1* regulates at least one important physiological function (i.e. cell proliferation), it is to be expected that the nucleotide sequence of *FEZ1* will be more highly conserved among organisms than less critical genes. Thus, it is contemplated that the isolated polynucleotide of the invention is useful not only for isolation and identification of primate and other mammalian *FEZ1* analogs, but also for isolating and identifying other vertebrate, other eukaryotic, and possibly any *FEZ1* analog. Preferably, when a non-human analog of *FEZ1* is to be isolated or identified, a plurality of isolated polynucleotides of the invention are used, each polynucleotide being complementary to a different portion of human *FEZ1*. Also preferably, at least one isolated polynucleotide of the invention is complementary to a portion of human *FEZ1* which can be expected to be particularly conserved, such as the portion which encodes the leucine-zipper region of Fez1 protein.

Also contemplated is a manufacture comprising a plurality of isolated polynucleotide probes of the invention fixed in an ordered array on a surface. Such manufactures are colloquially known as 'gene chips.' Each of the plurality of probes anneals with high stringency with a portion of the human *FEZ1* gene. By including probes which differ by a single nucleotide residue within the corresponding portion of the *FEZ1* gene, nucleic acids which comprise different nucleotide residues at that position within the *FEZ1* gene can be differentiated. Thus, using methods well known in the art, missense and deletion mutations in the *FEZ1* sequence can be detected. Furthermore, by incorporating into the array probes which bind with high affinity with sequential portions of the wild type *FEZ1* gene, wherein each sequential portion includes one nucleotide residue not included within the previous sequential portion, the nucleotide sequence of all, or any portion, of the *FEZ1* gene can be determined. Preferably, the wild type human *FEZ1* gene sequence which is used is SEQ ID NO: 1. An analogous ordered array can be designed to detect mRNA sequence alterations, preferably using SEQ ID NO: 2 or SEQ ID NO: 3 as the wild type human *FEZ1* mRNA sequence. Manufactures of this type are analogous to the GeneChip™ devices made by Affymetrix, Inc. (Santa Clara, CA), which comprise pluralities of primers which bind with high stringency to, for example, portions of the human *p53* gene or to portions of the HIV-1 protease or reverse transcriptase genes. Methods for making and using such manufactures have been described elsewhere, and need only be modified by the skilled artisan to include the *FEZ1* gene sequences described in the present disclosure (Wallraff et al., February 1997, Chemtech 22-23; Lockhart et al., 1996, Nature Biotechnol. 14:1675-1680; Pease et al., 1994, Proc. Natl. Acad. Sci. USA 91:5022-5026; Fodor et al., 1993, Nature 364:555-556).

One or more isolated polynucleotides of the invention can also be used as primers for replication or amplification of all or a portion of a nucleic acid comprising all or part of a human *FEZ1* gene or a non-human *FEZ1* analog. The nucleic acid may, for example, be either strand of a human genome, a human chromosome, a fragment of a human genome, or all or a portion of a non-human

genome, or it can be an mRNA generated by transcription of a human *FEZ1* gene or a non-human analog thereof or either strand of a cDNA generated using such an mRNA. In light of the present disclosure, the skilled artisan can replicate or amplify substantially any nucleic acid comprising a portion homologous with or complementary to all, or a portion, of a human *FEZ1* gene, such as that having the nucleotide sequence SEQ ID NO: 1. Methods of DNA transcription, RNA reverse transcription, DNA replication, polymerase chain reaction (PCR), and the like are well known and not described beyond citation to the following standard references (Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York; Ausubel et al., 1992, Current Protocols in Molecular Biology, John Wiley & Sons, New York; Gerhardt et al., eds., 1994, Methods for General and Molecular Bacteriology, American Society for Microbiology, Washington, DC). Methods of amplifying genomic regions which flank an already-sequenced genomic region are likewise known and are included within the scope of the invention insofar as amplification of genomic regions which flank a human *FEZ1* gene or a non-human analog thereof are concerned.

When a pair of isolated polynucleotides of the invention is to be used to amplify all or a portion of a human *FEZ1* gene, a transcript thereof, or a cDNA generated using such a transcript, the polynucleotides should be selected such that one polynucleotide anneals with one strand with high stringency near one end of the region to be amplified and the other polynucleotide anneals with the other strand with high stringency near the other end of the region to be amplified, as is well known in PCR methods. Of course, as is likewise well known, if the nucleic acid to be amplified is an mRNA or other RNA molecule, then a cDNA complementary to the mRNA must be made prior to performing a PCR reaction.

Substantially any region of the human *FEZ1* gene, or of a non-human analog thereof, can be amplified using one or more isolated polynucleotides of the invention. In one embodiment, polynucleotides which anneal with high stringency with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 nucleotide residues near

opposite ends and on opposite strands of the human *FEZ1* gene are used to amplify the entire human *FEZ1* gene, or a non-human analog thereof, from one or more portions of a human or non-human genome.

In another embodiment, one or more pairs of isolated polynucleotide primers are selected, each of which pairs of primers comprises a first primer which anneals with high stringency with an intronic portion which flanks the 5'- or 3'-end of an exon on the coding strand of a nucleic acid encoding the exon and a second primer which anneals with high stringency with an intronic portion which flanks the 3'- or 5'-end, respectively, of the same exon on the non-coding strand of the nucleic acid. Optionally, each of the two primers of each pair is adjacent the designated end of the exon. Thus, according to this method, amplification of a nucleic acid encoding at least one exon of the human *FEZ1* gene, or a non-human analog thereof, using one or more pairs of primers results in amplification of one or more exon sequences of the gene or analog, optionally not including any intronic sequence. It is understood that amplification of both an exon sequence and the intronic sequences which flank it can be more informative than amplification of exon sequences alone, since sequence alterations which appear in an intron but nonetheless affect the amino acid sequence of the encoded protein (e.g. mutations which affect mRNA splicing) can be revealed.

In another embodiment of the amplification methods of the invention, pairs of isolated polynucleotide primers of the invention are selected such that amplification of the wild type human genomic *FEZ1* region (e.g. SEQ ID NO: 1), the corresponding wild type mRNA, or a cDNA generated from wild type human *FEZ1* mRNA using these pairs of primers yields a mixture of amplification products having determined lengths. Fractionation of these amplification products by size (e.g. by gel electrophoresis or by chromatography) will yield a characteristic pattern for the wild type sequence. Amplification of the same nucleic acid obtained from an individual having a mutation which affects the length or presence of any of the amplification products will yield a different pattern than the wild type pattern, and the presence of the mutation in the individual can thus be identified.

In still another embodiment of the amplification methods of the invention, pairs of isolated polynucleotide primers of the invention are selected in order to amplify regions of a nucleic acid encoding human Fez1 protein, or a non-human analog thereof, which are known to be altered (i.e. wherein a deletion or missense mutation are known to occur) in tumor cells. Several such regions are described herein in Example 1, and primers useful for amplifying these regions are included in the invention. Identification of the presence of such alterations is an indication that the cell or tissue from which the nucleic acid was obtained is cancerous. Examples of primers useful in this embodiment include, for example, primer pairs G12 and G13, G14.2 and G15, and G16 and IntABR for amplifying the coding region of exon 1, primer pairs IntABF and G17, G20 and G21, and G32 and IntBCR for amplifying the coding region of exon 2, and primer pairs IntBCF and Mut6, G1 and G2, G75 and G82, G5 and G6, and G7 and G8 for amplifying the coding region of exon 3. These primers have the nucleotide sequences listed in the following table.

Primer Nucleotide Sequence Table

Primer	Nucleotide Sequence (5'→3')	SEQ ID NO
G12	GCTGCCACAGCCTTTCCAAGACC	22
G13	TACCGGTTGAGCTTCTTGAGGTG	23
G14.2	ACAGCTTCCACAGCAAGCACTGC	24
G15	ATTGGAGAAGGGCATGAGCTT	25
G16	TGGACTTTGACCCGTCCACACC	26
IntABR	GTTTCCAACCCACTTACCCTTGC	27
IntABF	GCAGGGGAGGCATGAGTCACC	28
G17	GGCTTCAGCTCCTGCTCCTTGG	29
G20	ACAACATCACCCAGGGCATCGTC	30
G21	CCTCCAGCTCGTCCCTGCAGC	31
G32	ACTGCAGCTTCAGCAGGAGAAGC	32
IntBCR	CTGACCACCCAAACCCATGAGC	33
IntBCF	TCACCTCTTGGCACTCTGTCTCC	34
Mut6	CAGGTCCTGGGTCCTCAGCTC	35
G1	TGAACGCCAAGGCTAGCGAGATC	36
G2	GCTCCTGCAGCTCCTGCTCCAG	37
G75	CCCACCTTCCCCGAGGACGTC	38
G82	AGCCCGAGGACATCTGGTCATGG	39
G5	CCTGCCCTGCAGCGGGAGCTGGAG	40
G6	AGCTGCTGCAGGGCCTTCTCCAG	41
G7	CAGTACCAGAAACAGCTGCAGCAGAGC	42
G8	CCCTGCCTCCCAGTGCCAGGTC	43

Use of isolated polynucleotide primers comprising both a fluorophore and a molecule capable of quenching fluorescence of the fluorophore for quantitative amplification of nucleic acids homologous with all or part of the human *FEZ1* gene is contemplated. Use of such labeled primers has been described elsewhere (Livak et al., 1995, "Guidelines for Designing TaqMan™ Fluorogenic Probes for 5' Nuclease Assays", Perkin Elmer, Norwalk, CT; U.S. Patent No. 5,210,015; U.S. Patent No. 5691,146; Heid et al., 1996, Genome Res. 6:986-994).

The isolated polynucleotide of the invention can also be used as an antisense oligonucleotide (ASO) to inhibit expression of a human *FEZ1* gene or a non-human analog thereof. As is well known in the art, an ASO can be complementary to either the coding or non-coding strand of a gene. ASOs are used by delivering the ASO to the interior of a cell, and preferably to the interior of the nucleus of a cell, whereby the ASO is enabled to interact with one or more nucleic acids which encode a protein. When an isolated polynucleotide of the invention is used as an ASO, it binds with high stringency with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 consecutive nucleotide residues of at one strand of a human *FEZ1* gene, such as that having the sequence SEQ ID NO: 1, even if the ASO is used *in vitro* or in a non-human animal. When the recipient of the ASO is a human cell, either *in vitro* or *in vivo*, the isolated polynucleotide ASO of the invention is preferably substantially homologous, and more preferably completely homologous with at least 20, 21, 22, ..., 30, 31, 32, ..., 40, 41, 42, ..., or 50 consecutive nucleotide residues of the human *FEZ1* gene (SEQ ID NO: 1). Furthermore, the isolated polynucleotide ASO is preferably substantially or completely homologous with the translation start site, the transcription start site, an exon-intron boundary for splicing immature mRNA, or a coding sequence of the human *FEZ1* gene. Other preferred ASO are complementary to or homologous with and approximately about as long as the *FEZ1* ORF (SEQ ID NO: 3) or a significant portion (e.g. 100-500 nucleotides) thereof. ASOs can be administered either in a single-stranded or double-stranded form, although the single-stranded form is

preferable. ASOs can be administered to an animal or a cell either in the form of a pharmaceutical composition comprising the ASO, as described herein.

The isolated polynucleotide of the invention can also be used as a template for expression of human Fez1 protein, either *in vitro* or *in vivo*. When *in vitro* expression of Fez1 protein is desired, it is preferable to use an isolated polynucleotide which does not comprise the intronic regions of *FEZ1*, such as an isolated polynucleotide which comprises a portion which is complementary to at least one strand of a cDNA generated using a spliced human mRNA encoding Fez1 protein (e.g. a cDNA having the nucleotide sequence SEQ ID NO: 2 or SEQ ID NO: 3). Methods and compositions useful for *in vitro* expression of protein from a nucleic acid are well known in the art and are described elsewhere (e.g. Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York; Ausubel et al., 1992, Current Protocols in Molecular Biology, John Wiley & Sons, New York).

When the isolated polynucleotide of the invention is used as a template for expression of human Fez1 protein *in vivo*, the isolated polynucleotide has a sequence substantially homologous with at least nucleotide residues 112-456, nucleotide residues 1707-2510, and nucleotide residues 4912-5550 of at least one strand of SEQ ID NO: 1. If the cell in which Fez1 protein is expressed is a mammalian cell, and especially if it is a human cell, it is not necessary to delete the intronic regions of *FEZ1* from the isolated polynucleotide. Preferably, however, the intronic regions of *FEZ1* are deleted from the isolated polynucleotide prior to providing it to the cell.

When the isolated polynucleotide of the invention is used as a template for expression of human Fez1 protein *in vivo*, the isolated polynucleotide is preferably provided to a cell in the form of an expression vector, wherein the region(s) encoding Fez1 protein are operably linked with a promoter region. The promoter region can be the human *FEZ1* promoter region, or it can be substantially any other promoter region. In various embodiments, the promoter region of the expression vector is a constitutive promoter, an inducible promoter, or a tissue-specific promoter. Numerous constitutive promoters are known in the art and included within the scope of the invention.

Exemplary constitutive promoters include, for example, a retroviral LTR promoter, the cytomegalovirus immediate early promoter, the SV40 early promoter, the herpes simplex virus thymidine kinase promoter, an adenovirus-based promoter, elongation factor 1 alpha promoter, SV40-HTLV-1 LTR fusion promoter, and the CMV-beta actin enhancer fusion promoter.

Operable linkage of an isolated polynucleotide of the invention with an inducible promoter permits controlled expression of Fez1 protein following delivery of the expression vector to a cell. Such controlled expression is modulated by providing an inducer of the promoter to, or withholding or removing such an inducer from, the cell. An example of an inducible promoter which can be operably linked to an isolated polynucleotide of the invention is a tetracycline promoter, which is well known in the art to be an inducible promoter.

Operable linkage of an isolated polynucleotide of the invention with a tissue-specific promoter permits localization of expression of Fez1 protein to a tissue of interest, thereby minimizing any side effects which can be associated with non-tissue-specific expression of Fez1 protein. The tissue-specific promoter may, for example, be selected from the group consisting of an epithelium-specific promoter, a tumor-specific promoter, a breast-specific promoter, a prostate-specific promoter, and an esophagus-specific promoter. By way of example, the prostate-specific antigen promoter can be operably linked to an isolated polynucleotide of the invention in order to achieve prostate-specific expression of Fez1 protein.

The isolated polynucleotide of the invention can be provided to a cell, either *in vitro* or *in vivo*, using a wide variety of gene delivery vectors. The identity of the vector is not critical; substantially any vector known in the art for delivering a nucleic acid to the interior of a cell can be used for this purpose. Exemplary vectors include, but are not limited to naked DNA vectors, plasmids, condensed nucleic acids, projected nucleic acid-coated micro- or nano-particles, and virus vectors.

The invention also includes an animal cell which comprises an exogenous DNA molecule having at least one portion which is substantially

homologous with at least the coding regions of the human *FEZ1* gene. For example, the exogenous DNA molecule can comprise one, two, three, or more regions which, individually or together are substantially homologous with nucleotide residues 112-456, nucleotide residues 1707-2510, and nucleotide residues 4912-5550 of at least one strand of SEQ ID NO: 1. Preferably, the exogenous DNA molecule comprises one region that is substantially homologous with at least one strand of SEQ ID NO: 2. More preferably, the exogenous DNA molecule is completely homologous with the coding regions of the human *FEZ1* gene. Also preferably, the exogenous DNA molecule comprises a promoter operably linked with the *FEZ1* coding region(s), whereby Fez1 protein is expressed in cells comprising the exogenous DNA molecule.

The cell can be a human cell, a non-human animal cell, or a non-animal cell, such as a plant cell, a yeast cell, a fungus cell, or a bacterium. The cell can likewise be a cultured cell, a cell within the body of an animal, or a cell which is removed from the body of an animal for the purpose of providing the exogenous DNA molecule prior to returning the cell to the body of the same or a different animal.

The invention further relates to an animal comprising a cell which comprises an exogenous DNA molecule having at least one portion which is substantially homologous with at least the coding regions of the human *FEZ1* gene. Preferably, the animal is a human which comprises a tissue which lacks a copy of the human wild type *FEZ1* gene, such as certain tumor tissues. Such animals (e.g. mice) can be made by disrupting the *FEZ1* gene in the animal using known gene targeting methods. By way of example, exon 1 of *FEZ1* can be replaced with a neomycin-resistance cassette. Embryonic stem cells of the animal are transfected using the targeting construct DNA vector, and cells are selected for neomycin resistance. In these cells, homologous recombination between the targeting construct DNA and one of the animal's genomic copy of the *FEZ1* gene occurs. In rare instances, recombination of both *FEZ1* copies can occur, but it is anticipated that most, if not all selected cells will be heterozygous for recombined *FEZ1*-neomycin resistance gene, and will develop as heterozygous adult animals. These heterozygous animals exhibit

characteristics attributable to animals having only a single functional *FEZ1* gene per cell, such as abnormal cell or tissue differentiation, abnormal cell proliferation, increased incidence of cancer and other cell proliferative disorders, and uncontrolled gene expression. Furthermore, mating of heterozygous *FEZ1* animals yields animals homozygous for the recombined *FEZ1*-neomycin resistance gene (i.e. *FEZ1* "knockout" animals). These *FEZ1* knockout animals exhibit traits characteristics attributable to the lack of a functional *FEZ1* gene in the cells of the animal. Such characteristics include, for example, abnormal cell or tissue differentiation, abnormal cell proliferation, increased incidence of cancer and other cell proliferative disorders, and uncontrolled gene expression.

The Isolated Fez1 protein of the Invention

The invention also relates to an isolated Fez1 protein. The putative amino acid sequence of human Fez1 protein (SEQ ID NO: 4) is shown in Figure 5D. Preferably, the isolated human Fez1 protein is substantially purified. The isolated human Fez1 protein can be in the form of a suspension of the native or denatured protein in a liquid such as water, a buffer, or the like, a lyophilized powder, an immunogenic composition comprising the protein and one or more adjuvants or immunogenicity enhancers such as are known in the art, or a pharmaceutical composition as described elsewhere herein.

The isolated Fez1 protein of the invention can be made by a variety of techniques. For example, the protein can be expressed in an *in vitro* expression mixture using an isolated polynucleotide of the invention. The isolated polynucleotide of the invention can also be operably linked with a constitutive or other promoter, and the Fez1 protein overexpressed in a human or non-human cell, and subsequently purified therefrom. Alternately, the Fez1 protein can be purified using, for example, standard chromatographic techniques from a naturally occurring source of human Fez1 protein (e.g. normal human brain or testes tissue).

The invention also includes fragments of the isolated Fez1 protein of the invention. Such fragments can be generated, for example, by expressing an isolated

polynucleotide of the invention, wherein the polynucleotide encodes only a portion of human Fezl protein, or by proteolytic degradation of human Fezl protein.

Although it is preferred that the isolated human Fezl protein has an amino acid sequence completely homologous with SEQ ID NO: 4, the amino acid sequence of the isolated Fezl protein can comprise one or more conservative amino acid substitutions relative to SEQ ID NO: 4).

For example, certain amino acids of the human Fezl protein can be substituted for other amino acids without appreciably affecting the biological activity of the protein. Preferably, the amino acid sequence of the isolated Fezl protein of the invention is substantially homologous with SEQ ID NO: 4. The hydropathic index of naturally occurring Fezl amino acid residues can be compared with those of potential substitute amino acid residues. The significance of amino acid hydropathic index similarity between naturally occurring and potential substitute amino acid residues, as it relates to retention of biologic function of a protein is generally understood in the art. It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each naturally occurring amino acid residue has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics, as described (Kyte et al., 1982, J. Mol. Biol. 157:105). These hydropathic index values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5);glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5). Amino acid residues can be substituted in place of other amino acid residues which having a similar hydropathic index without significantly affecting biological activity of the protein. Preferably, the substitute amino acid residue has a hydropathic index which differs from the hydropathic index of the naturally occurring

amino acid residue by less than 2.0, preferably by less than 1.0, and more preferably by less than 0.5. For example, if the hydropathic index of a naturally occurring amino acid residue is 1.8, then a substitute amino acid residue should have a hydropathic index in the range from 3.8 to -0.2, preferably in the range from 2.8 to 0.8, and more preferably in the range from 2.3 to 1.3.

An alternate method can be used to predict amino acid residues which can be substituted in place of naturally occurring Fez1 amino acid residues in regions of the Fez1 protein which are predicted to interact with other molecules (e.g. the leucine zipper region of Fez1, which is thought to interact with DNA). This method has been described in the art (Hoop et al., 1981, Proc. Natl. Acad. Sci. USA 78:3824), and involves assigning the following hydrophilicity values to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0); glutamate (+3.0); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); proline (0.0); threonine (-0.4); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). Amino acid residues can be substituted in place of other amino acid residues having a similar hydrophilicity value without significantly affecting biological activity of the protein. Preferably, the substitute amino acid residue has a hydrophilicity value which differs from the hydrophilicity value of the naturally occurring amino acid residue by less than 2.0, preferably by less than 1.0, and more preferably by less than 0.5. For example, if the hydrophilicity value of a naturally occurring amino acid residue is 1.8, then a substitute amino acid residue should have a hydrophilicity value in the range from 3.8 to -0.2, preferably in the range from 2.8 to 0.8, and more preferably in the range from 2.3 to 1.3.

As outlined above, amino acid substitutions can be based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. For example, conservative amino acid substitutions can include substitutions within the following groups:

glycine, alanine;

valine, isoleucine, leucine;

aspartic acid, glutamic acid;

asparagine, glutamine;

serine, threonine;

lysine, arginine;

phenylalanine, tyrosine.

Modifications (which do not normally alter primary sequence) include *in vivo*, or *in vitro* chemical derivatization of polypeptides, *e.g.*, acetylation, or carboxylation. Also included are modifications of glycosylation, *e.g.*, those made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing or in further processing steps; *e.g.*, by exposing the polypeptide to enzymes which affect glycosylation, *e.g.*, mammalian glycosylating or deglycosylating enzymes. Also embraced are sequences which have phosphorylated amino acid residues, *e.g.*, phosphotyrosine, phosphoserine, or phosphothreonine.

Also included are polypeptides which have been modified using ordinary molecular biological techniques so as to improve their resistance to proteolytic degradation or to optimize solubility properties or to render them more suitable as a therapeutic agent. Analogs of such polypeptides include those containing residues other than naturally occurring L-amino acids, *e.g.*, D-amino acids or non-naturally occurring synthetic amino acids. The isolated Fez1 protein of the invention, and fragments thereof, are not limited to products of any of the specific exemplary processes listed herein.

It will be appreciated, of course, that the isolated Fez1 proteins, and fragments thereof, can incorporate amino acid residues which are modified without affecting activity. For example, the termini can be derivatized to include blocking groups, i.e. chemical substituents suitable to protect and/or stabilize the N- and C-termini from "undesirable degradation", a term meant to encompass any type of enzymatic, chemical or biochemical breakdown of the compound at its termini which is

likely to affect the function of the compound (e.g. as an anti-proliferative agent) by sequential degradation of the compound at a terminal end thereof.

Blocking groups include protecting groups conventionally used in the art of peptide chemistry which will not adversely affect *in vivo* activities of the Fez1 proteins or fragments thereof. For example, suitable N-terminal blocking groups can be introduced by alkylation or acylation of the N-terminus. Examples of suitable N-terminal blocking groups include C_1-C_5 branched or non-branched alkyl groups, acyl groups such as formyl and acetyl groups, as well as substituted forms thereof, such as the acetamidomethyl (Acm) group. Desamino analogs of amino acids are also useful N-terminal blocking groups, and can either be coupled to the N-terminus of the peptide or used in place of the N-terminal residue. Suitable C-terminal blocking groups, in which the carboxyl group of the C-terminus is either incorporated or not, include esters, ketones, and amides. Ester or ketone-forming alkyl groups, particularly lower alkyl groups such as methyl, ethyl and propyl, and amide-forming amino groups such as primary amines (-NH_2), and mono- and di-alkylamino groups such as methylamino, ethylamino, dimethylamino, diethylamino, methylethylamino, and the like are examples of C-terminal blocking groups. Descarboxylated amino acid analogues such as agmatine are also useful C-terminal blocking groups and can be either coupled to the peptide's C-terminal residue or used in place of it. Further, it will be appreciated that the free amino and carboxyl groups at the termini can be removed altogether from the Fez1 proteins, or fragments thereof, to yield desamino and descarboxylated forms thereof without affect on biological activity.

Other modifications can also be incorporated without adversely affecting biological (e.g. anti-proliferative) activity and these include, but are not limited to, substitution of one or more of the amino acids in the natural L-isomeric form with amino acids in the D-isomeric form. Thus, the Fez1 proteins, or fragments thereof, can include one or more D-amino acid residues, or can comprise amino acids which are all in the D-form. Retro-inverso forms of proteins peptides in accordance

with the present invention are also contemplated, for example, inverted peptides in which all amino acids are substituted with D-amino acid forms.

Acid addition salts of the Fez1 proteins, or fragments thereof, of the present invention are also contemplated as functional equivalents. Thus, a protein or peptide in accordance with the present invention can be treated with an inorganic acid such as hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, and the like, or an organic acid such as an acetic, propionic, glycolic, pyruvic, oxalic, malic, malonic, succinic, maleic, fumaric, tartaric, citric, benzoic, cinnamic, mandelic, methanesulfonic, ethanesulfonic, p-toluenesulfonic, or salicylic acid to provide a water soluble salt of the peptide which is suitable for use as an anti-proliferative agent.

The isolated Fez1 protein of the invention, or a fragment thereof, can be used to generate polyclonal or monoclonal antibodies using known methods. As is well known, administration of the Fez1 protein of the invention to an animal can induce a soluble immune response against the protein or fragment in the animal. Preferably, the protein or fragment is mixed with an adjuvant or other immune system enhancer. Such adjuvants include, but are not limited to, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, and polyanions, other peptides, and oil emulsions. Antibodies which bind specifically with the Fez1 protein or fragment can be identified and isolated using well known methods (see, e.g. Harlow et al., 1988, Antibodies: A Laboratory Manual, Cold Spring Harbor, New York). Likewise, immortal hybridomas can be generated using known methods to provide a supply of such antibodies.

Diagnostic Methods of the Invention

As described herein, reduced or no expression of the human *FEZ1* gene has been demonstrated in numerous cancer cell lines and tumor samples. These data indicate that assessment of the level of *FEZ1* gene expression in a cell or tissue of a human can indicate the cancerous state of the cell or tissue. Diagnostic techniques based on this relationship have the advantage that tumorigenesis can be detected in cells and tissues at an early stage, before other physiological changes associated with

cancers can be detected in the same cells or tissues. Furthermore, these diagnostic techniques can be used to confirm or refute a preliminary diagnosis of tumorigenesis made by visual or cytological examination of potentially cancerous tissue.

The diagnostic methods described in this section are useful for diagnosing cancer in a body tissue of a human, particularly where the body tissue is an epithelial tissue. By way of example, the body tissue can be selected from the group consisting of a gastrointestinal tissue, esophageal tissue, gastric tissue, colon tissue, prostate tissue, breast tissue, a hematopoietic tissue, lung tissue, melanoma tissue, cervical tissue, and ovarian tissue.

B12 The invention includes a method of determining the cancerous status of a sample tissue. This method comprises comparing *FEZ1* expression in the sample tissue with *FEZ1* expression in a control tissue of the same type. Decreased *FEZ1* expression in the sample tissue, relative to *FEZ1* expression in the control tissue, is an indication that the sample tissue is cancerous. The sample tissue can be a phenotypically abnormal tissue (e.g. a biopsy sample obtained from a potentially cancerous lesion in a human tissue such as breast or prostate), or it can be a phenotypically normal tissue. The control tissue is a non-cancerous tissue of the same type, and can be obtained from the same human from whom the sample tissue was obtained, or from one or more humans different than the one from whom the sample tissue was obtained. If a body of data exist or are created, from which a representative value for expression of *FEZ1* in non-cancerous tissue of the same type as the sample tissue, then *FEZ1* expression in the sample tissue can be compared with this representative value, rather than performing a separate determination of *FEZ1* expression in the same or a different human.

Expression of *FEZ1* in the sample tissue is compared with *FEZ1* expression in a control tissue (or data set) by comparing the relative amounts of at least one indicator in the sample tissue and in the control tissue (or data set). The indicator which is used can be any indicator which can be correlated with transcription of the *FEZ1* gene in the tissue or with translation of this transcript is such tissue. For

example, the indicator can be selected from the group consisting of a *FEZ1* mRNA, a cDNA prepared using a *FEZ1* mRNA, a DNA prepared by amplification of either of these, and Fez1 protein.

The invention also includes another method of determining the cancerous status of a sample tissue. This method comprises comparing the nucleotide sequence of a *FEZ1*-associated polynucleotide obtained from the sample tissue with the nucleotide sequence of a control *FEZ1*-associated polynucleotide. A difference between the nucleotide sequence of the *FEZ1*-associated polynucleotide obtained from the sample tissue and the nucleotide sequence of the control *FEZ1*-associated polynucleotide is an indication that the sample tissue is cancerous. The *FEZ1*-associated polynucleotide may, for example, be one selected from the group consisting of at least a portion of a chromosome, a non-spliced mRNA, a partially spliced mRNA, a fully spliced mRNA, a cDNA prepared using a non-spliced mRNA, a cDNA prepared using a partially spliced mRNA, a cDNA prepared using a fully spliced mRNA, and a DNA prepared by amplification of any of these. By way of example, the *FEZ1*-associated polynucleotide can be DNA prepared by amplification of a cDNA prepared using a fully spliced mRNA obtained from a human, in which case, the control *FEZ1*-associated polynucleotide should be a DNA having the sequence SEQ ID NO: 3. Further by way of example, the *FEZ1*-associated polynucleotide can be a DNA prepared by amplification of at least a portion of chromosome 8 of a human, in which case, the control *FEZ1*-associated polynucleotide should be a DNA having the sequence SEQ ID NO: 1.

According to this method, the sample and control tissues can both be obtained from the same human, in which case, the sample tissue should be a phenotypically abnormal portion of a body tissue of a human or a portion of the tissue in which tumorigenesis is anticipated, and the control *FEZ1*-associated polynucleotide should be obtained from a phenotypically normal portion of the same body tissue or from a portion of the tissue in which tumorigenesis is not anticipated. The sample and control tissues can also be obtained from the same tissue, but from different humans, in

which case the control tissue should be obtained from a human whose relevant tissue is not cancerous. Alternately, as described above, the 'control tissue' can be a body of data collected from the relevant type of tissue obtained from a plurality of humans in whom the relevant tissue was not cancerous. In this case, only the nucleotide sequence of the sample *FEZ1*-associated polynucleotide need be determined experimentally, and this sequence can be compared with a consensus or other sequence indicated by the body of data. For example, the *FEZ1* gene sequence described herein (SEQ ID NO: 1), the *FEZ1* cDNA sequence described (SEQ ID NO: 2), or the *FEZ1* ORF sequence described herein (SEQ ID NO: 3) can be used as the control *FEZ1*-associated polynucleotide sequence.

The invention includes yet another method of determining the cancerous status of a sample tissue. As described herein, certain mutations in the human *FEZ1* gene lead to production of transcripts from this gene which have lengths which are different from the length of the wild type *FEZ1* gene transcript. This method correlates this transcript length difference with a cancerous state in a sample tissue. This method comprises comparing the length of an *FEZ1*-transcript-associated polynucleotide obtained from the sample tissue with the length of a control *FEZ1*-transcript-associated polynucleotide. If the length of the *FEZ1*-transcript-associated polynucleotide obtained from the sample tissue is less than the length of the control *FEZ1*-transcript-associated polynucleotide, then this is an indication that the sample tissue is cancerous. The *FEZ1*-transcript-associated polynucleotide may, for example, be selected from the group consisting of a fully spliced mRNA, a cDNA prepared using a fully spliced mRNA, and a DNA prepared by amplification of either of these. In one embodiment of this method, the *FEZ1*-transcript-associated polynucleotide is DNA prepared by amplification of a cDNA prepared using a fully spliced mRNA obtained from a human, and the control *FEZ1*-transcript-associated polynucleotide is DNA having the sequence SEQ ID NO: 2.

In another embodiment of this method, the *FEZ1*-transcript-associated polynucleotide is fully spliced mRNA obtained from a human patient, and the control

FEZ1-transcript-associated polynucleotide is at least a portion of a nucleic acid which is complementary to SEQ ID NO: 2, whereby binding of the patient's mRNA and the control polynucleotide can be detected using standard RNA blot or Northern blot analytical techniques.

As in the methods described above, the sample and control *FEZ1*-transcript-associated polynucleotides can be obtained from the same or different humans, and the control *FEZ1*-transcript-associated polynucleotide can instead be a consensus or other relevant sequence described herein or formulated using *FEZ1*-transcript-associated polynucleotide sequences obtained from humans in whom the relevant tissue was not cancerous.

The invention includes still another method of determining the cancerous status of a sample tissue. This method comprises assessing *FEZ1* expression in the sample tissue. A substantial absence of *FEZ1* expression in the sample tissue is an indication that the sample tissue is cancerous. *FEZ1* expression can be assessed by assessing the presence or substantial absence of at least one indicator selected from the group consisting of a *FEZ1* mRNA, a cDNA prepared using a *FEZ1* mRNA, a DNA prepared by amplification of either of these, and Fez1 protein.

The invention also includes another method of determining the cancerous status of a sample tissue. This method comprises detecting abnormal splicing of a *FEZ1* transcript in the sample tissue. Abnormal splicing of the *FEZ1* transcript is an indication that the sample tissue is cancerous. Abnormal splicing of a *FEZ1* transcript may, for example, be detected by assessing the ability of at least one exon boundary polynucleotide probe to anneal with a *FEZ1*-transcript-associated polynucleotide with high stringency. Such an exon boundary polynucleotide probe is capable of annealing with high stringency with terminal portions of two sequential *FEZ1* exons when the terminal portions are adjacent, but not when the terminal portions are not adjacent. By way of example, such an exon boundary polynucleotide probe can comprise two portions, one portion which binds with high stringency with the 3'-end of the first exon of a DNA, mRNA, or cDNA coding strand of *FEZ1*, and

another portion which binds with high stringency with the 5'-end of the second exon of a DNA, mRNA, or cDNA coding strand of *FEZ1*. If the two portions of the probe are adjacent, then the probe will bind with high stringency with an mRNA, or with the coding strand of a cDNA generated using that mRNA, only if the two exons are adjacent in the mRNA or cDNA. Thus, if the mRNA has been abnormally spliced, such that the first and second exons of *FEZ1* are not adjacent in the spliced mRNA (and are therefore not adjacent in the corresponding cDNA), then the probe will not bind with the mRNA, or the corresponding cDNA, with high stringency. Design of such primers is well within the level of ordinary skill in the art, in light of the present disclosure.

Immunohistological Diagnostic Methods

The invention also includes an immunohistological method for detecting expression of Fez1 protein in a cell or tissue sample obtained from a human patient. This method involves use of an antibody preparation (e.g. a monoclonal or polyclonal antibody preparation) generated using the isolated Fez1 protein of the invention (or a fragment thereof) according to standard antibody generating methods. This preparation contains one or more types of antibodies which bind specifically with human Fez1 protein. The antibody preparation is contacted with the cell or tissue sample, and the Fez1-binding antibodies are labeled, either prior to or after contact with the sample. Non-specifically bound antibody is washed from the sample, and the presence of labeled antibody in or on the sample is assessed. The presence of labeled antibody is an indication that the sample comprises human Fez1 protein. Thus, this immunohistological method can be used to detect Fez1 expression, or a decrease of such expression, which is associated with an enhanced likelihood of tumorigenesis, for example.

Therapeutic Methods of the Invention

Abnormal expression of the human *FEZ1* gene is not merely a symptom of epithelial and other cancers in human tissues. It is also a contributing cause, and possibly the sole cause in some instances of tumorigenicity in those tissues.

Inactivation of all genomic copies of the *FEZ1* gene in one or more cells of a human tissue, especially an epithelial tissue, can lead to abnormal proliferation of those cells. Normal control of cell proliferation can be restored either by reactivating a genomic copy of the *FEZ1* gene in abnormally proliferating cells or by providing at least one exogenous source of Fez1 protein to abnormally proliferating cells. The exogenous source of Fez1 protein may, for example, be a nucleic acid encoding Fez1 protein or a composition comprising Fez1 protein. The exogenous source of Fez1 protein can be provided to the cells prior to tumorigenesis (i.e. for the purpose of inhibiting, delaying, or preventing tumorigenesis) or anytime after the onset of tumorigenesis (i.e. for the purpose of inhibiting, delaying, or preventing further abnormal proliferation of tumor cells or for the purpose of reversing abnormal proliferation).

The invention thus includes a method of modulating proliferation of a human cell having an altered *FEZ1* gene. This method comprises providing to the cell an exogenous source of Fez1 protein. When the protein is provided to the cell, abnormal proliferation of the cell is inhibited, delayed, or prevented.

The cell to which the exogenous source of Fez1 protein is provided can have one, two, or even more copies of an altered *FEZ1* gene, and can have no normally-functioning copy of this gene. It is contemplated that, in most instances, this method will be employed in situations in which it is recognized that a tissue in a human patient comprises cells which do not express a wild type *FEZ1* gene, or which express it at an abnormally low level. Expression of *FEZ1* in a cell is considered to be abnormally low when less than about 50, 49, 48, ..., 40, 39, 38, ..., 30, ..., 20, ..., 10, ... 5, ..., or 1 percent of the level of expression of *FEZ1* observed in non-cancerous cells of the same type is observed in the cell. The cell may, for example, be a cell which is recognizable as a tumor cell, a cell which is abnormally proliferating but not yet recognizable as a tumor cell, a metastatic cancer cell, a cell which is predisposed to abnormal proliferation but not yet recognizable as a tumor cell, or a cell which has an altered *FEZ1* gene but is not proliferating abnormally at the time the exogenous source of Fez1 protein is provided to the cell. The cell is preferably an epithelial cell, such as

a breast epithelial cell, a prostate epithelial cell, an esophageal epithelial cell, a lung epithelial cell, or an epidermal epithelial cell.

The altered *FEZ1* gene may, for example, be one which is not transcribed in the cell, one which is transcribed to generate a transcript that is incorrectly spliced, one which comprises at least one mutation which reduces or abolishes the normal function of Fez1 protein, one which is transcribed but not translated, or one which has been partially or deleted from the genome of the cell.

The exogenous source of Fez1 protein may, for example, be a composition comprising an isolated human Fez1 protein of the invention, as described herein. Alternatively, the Fez1 protein can be a functional fragment or analog of Fez1 protein (i.e. a fragment of Fez1 or a peptidomimetic having structure similar to all or a portion of Fez1 protein, wherein the fragment or analog exhibits one or more of the physiological activities of Fez1 protein, such as inhibition of tubulin polymerization). The Fez1 protein is preferably a human Fez1 protein or a human Fez1 protein having one or more conservative amino acid residue substitutions. Preferably, the amino acid sequence of the Fez1 protein is completely homologous with the amino acid sequence of the Fez1 protein normally encoded by the *FEZ1* gene of the cell. In one embodiment, the amino acid sequence of the Fez1 protein is SEQ ID NO: 4. The isolated Fez1 protein provided to the cell may, as described herein, be expressed *in vitro*, isolated from an organism which has been transformed with a *FEZ1* gene, or isolated from a naturally-occurring source. For example, the Fez1 protein can be isolated from cultured cells of a patient for provision to other cells of the same patient, either *in vivo* or *ex vivo*. Further by way of example, the Fez1 protein can be isolated from cultured human or bacterial cells which have been transformed using an expression vector comprising a polynucleotide encoding at least the coding portion of a human *FEZ1* gene (e.g. SEQ ID NO: 1, SEQ ID NO: 2, or SEQ ID NO: 3), and preferably at least the coding portion of a human *FEZ1* gene obtained from the patient to whom the Fez1 protein is to be administered.

As described herein, the Fez1 protein can be administered to a human in numerous pharmaceutical compositions. Preferably, the composition is one which is known in the art for providing proteins to the interior of a cell (e.g. liposomes, membrane vesicles, microspheres having an aqueous core, protein-coated projected particles, etc.).

The exogenous source of Fez1 protein can also, for example, be an expression vector comprising a polynucleotide having at least one coding region which encodes a functional Fez1 protein. When the polynucleotide is expressed in the cell, Fez1 protein is provided to the cell. Preferably, the polynucleotide encodes a human Fez1 protein or a human Fez1 protein having one or more conservative amino acid residue substitutions. Preferably, the amino acid sequence of the Fez1 protein is completely homologous with the amino acid sequence of the Fez1 protein normally encoded by the *FEZ1* gene of the cell. In one embodiment, the amino acid sequence of the Fez1 protein is SEQ ID NO: 4. In another embodiment, the polynucleotide comprises a portion having the nucleotide sequence SEQ ID NO: 2. Also preferably, the polynucleotide comprises a portion which is substantially homologous, and more preferably completely homologous, with the wild-type genomic sequence of the *FEZ1* gene of the patient to whose cell(s) the polynucleotide is provided. For example, the polynucleotide can comprise a portion which is substantially or completely homologous with SEQ ID NO: 1. The polynucleotide may, of course, be an isolated polynucleotide of the invention, as described elsewhere herein, so long as the isolated polynucleotide encodes a functional Fez1 protein.

Nucleic acid-containing vectors, including expression vectors, are well known in the art, as are methods of targeting such vectors such that they provide the nucleic acid of the vector preferentially or exclusively to cells of certain types or to cells located primarily or only within certain tissues. Exemplary expression vectors include both non-viral vectors (e.g. plasmids, naked DNA, DNA complexed with a polycation such as polylysine, and the like) and viral vectors such as retroviral, adenoviral, and adeno-associated viral vectors. The use of all such vectors is

contemplated, and the selection of an appropriate vector is within the level of ordinary skill in the art, in light of the disclosure provided herein, the size, composition, and characteristics of the nucleic acid, the symptoms and condition of the patient to whom the nucleic acid is to be provided, and the characteristics of the vector.

As described elsewhere herein, the polynucleotide can be an expression vector in which the portion(s) of the polynucleotide which encode the Fez1 protein is operably linked with a promoter. The promoter can be a constitutive promoter, an inducible promoter, a tissue-specific promoter, or substantially any other promoter, although mammalian, and particularly human, promoters are preferred. In one embodiment, the promoter of the expression vector is a normal human *FEZ1* promoter region. In another embodiment, the promoter is an inducible promoter, and this therapeutic method further comprises administering an inducer of the promoter to the cell to which the polynucleotide is provided. In another embodiment, the promoter is a tissue-specific promoter which normally promotes expression of genes operably linked therewith in an epithelial tissue. In another embodiment, an expressible portion of the *FEZ1* gene is contained in the expression vector and is operably linked with a genetic element which can be used to cease *FEZ1* expression. Numerous genetic elements of this type are known, including, for example, those associated with the Cre-loxP system (Pluck, Intl. J. Exp. Pathol.77:269-278; Li et al., 1997, Human Gene Ther. 8:1695-1700; Lewandoski et al., 1997, Nature Genet. 17:223-225; Russ et al., 1996, J. Virol. 70:4927-4932; Sakai et al., 1995, Biochem. Biophys. Res. Comm. 217:393-401; de Wit et al., 1998, Nucl. Acids Res. 26:676-678).

The invention also includes a method of preventing tumorigenesis in a human cell. This method comprises providing to the cell an expression vector comprising a polynucleotide having at least one coding region which encodes a functional Fez1 protein. Fez1 protein is thereby expressed in the cell, and tumorigenesis is thereby prevented in the cell. The cell may, for example, be one in which an altered *FEZ1* gene has been detected, a cell of a tissue in which an altered *FEZ1* gene has been detected, a normal cell in an individual predisposed to *FEZ1* gene

alteration (e.g. a human having a family history of *FEZ1* gene alterations), or a normal cell in a normal individual. Preferably, the cell is an epithelial cell. The polynucleotide can be any of those described herein for modulating proliferation of a human cell having an altered *FEZ1* gene.

The invention also relates to a method of reversibly inducing proliferation of a cell. This method comprises providing an inhibitor of *FEZ1* gene expression to the interior of the cell. Proliferation of the cell is induced when the inhibitor is present in the interior of the cell, but is not induced when the inhibitor is not present in the interior of the cell. This method is useful to promote proliferation of desirable cells, either *in vitro* or *in vivo*. Examples of situations in which it would be advantageous to induce cell proliferation include, but are not limited to, when a tissue has been grafted from a location in one animal to another location in the same or a different animal (e.g. a skin allograft or a bone marrow transplant), when a mixture of desirable and undesirable cells has been treated to remove or kill undesirable cells (e.g. radiation therapy or chemotherapy of a partially cancerous tissue), or when healing of a wounded tissue is desired (e.g. healing of a skin puncture or incision).

The inhibitor used in this method can be an ASO, such as one of the isolated polynucleotides of the invention, or it can be a compound identified using one of the screening methods of the invention as an inhibitor of *FEZ1* gene expression. If the inhibitor is capable of diffusing across the cell membrane, then it is not necessary to use a vector to deliver the inhibitor to the interior of the cell; otherwise, use of a vector to deliver the inhibitor to the interior of the cell. Any vector known in the art, such as any of those described herein, can be used for this purpose.

Use of an ASO is preferred for reversibly inhibiting *FEZ1* gene expression. Useful ASO compositions are described elsewhere herein. According to this method, the ASO may, for example, be administered to the cell in the form a naked nucleic acid, a nucleic acid complexed with a polycationic or other condensing agent, a nucleic acid vector such as a plasmid or a virus vector, or the like. The ASO can be provided to the interior of the cell directly, or an expression vector encoding the ASO

can be provided to the interior of the cell. When such an expression vector is used, it is preferred that the expression of the ASO be regulatable. By way of example, the polynucleotide encoding the ASO can be operably linked with an inducible promoter, whereby the ASO is produced only when the inducer of the promoter is provided to the cell. Alternately, the expression vector can be incapable of being replicated. Examples of such replication-deficient vectors include, but are not limited to, plasmids which lack an origin of replication and replication-deficient virus vectors (e.g. replication-deficient adenovirus vectors). The mechanism by which expression of the ASO is regulated is not critical; instead, it is important that expression of the ASO can be halted or severely limited when desired.

When an isolated polynucleotide of the invention or an isolated *FEZ1* protein of the invention is administered to an animal, such as a human, for diagnostic, therapeutic, or other purposes, the polynucleotide or protein is preferably in the form of a pharmaceutical composition.

The invention includes a method of inhibiting tumorigenesis in a human. This method comprising administering to the human a compound selected from the group consisting of an inducer of *FEZ1* gene expression, an enhancer of *FEZ1* gene expression, a inhibitor of Fez1 phosphorylation, an enhancer of phosphorylated-Fez1 dephosphorylation, an agent that inhibits binding of Fez1 with EF1-γ, and an agent that inhibits binding of Fez1 with tubulin.

Pharmaceutical Compositions of the Invention

The invention encompasses the preparation and use of medicaments and pharmaceutical compositions comprising either Fez-1 protein, or another compound described herein as an active ingredient. The isolated polynucleotide of the invention may, as described herein, be provided in the form of a nucleic acid vector, including, but not limited to, an expression vector.

The pharmaceutical compositions of the invention can consist of one or more active ingredients alone, in a form suitable for administration to a subject, or the

pharmaceutical composition can comprise one or more active ingredients and one or more pharmaceutically acceptable carriers, one or more additional ingredients, or some combination of these. Administration of one of these pharmaceutical compositions to a subject is useful for performing any of the methods of the invention, as described elsewhere in the present disclosure. The active ingredient can be present in the pharmaceutical composition in the form of a physiologically acceptable ester or salt, such as in combination with a physiologically acceptable cation or anion, as is well known in the art.

The formulations of the pharmaceutical compositions described herein can be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient into association with a carrier or one or more other accessory ingredients, and then, if necessary or desirable, shaping or packaging the product into a desired single- or multi-dose unit.

Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions which are suitable for ethical administration to humans, it will be understood by the skilled artisan that such compositions are generally suitable for administration to animals of all sorts. Modification of pharmaceutical compositions suitable for administration to humans in order to render the compositions suitable for administration to various animals is well understood, and the ordinarily skilled veterinary pharmacologist can design and perform such modification with merely ordinary, if any, experimentation. Subjects to which administration of the pharmaceutical compositions of the invention is contemplated include, but are not limited to, humans and other primates, mammals including commercially relevant mammals such as cattle, pigs, horses, sheep, cats, and dogs, birds including commercially relevant birds such as chickens, ducks, geese, and turkeys, fish including farm-raised fish and aquarium fish, and crustaceans such as farm-raised shellfish.

Pharmaceutical compositions that are useful in the methods of the invention can be prepared, packaged, or sold in formulations suitable for oral, rectal, vaginal, parenteral, topical, pulmonary, intranasal, buccal, ophthalmic, or another route of administration. Other contemplated formulations include projected nanoparticles, liposomal preparations, resealed erythrocytes containing the active ingredient, and immunologically-based formulations.

In addition to the active ingredient, a pharmaceutical composition of the invention can further comprise one or more additional pharmaceutically active agents.

Controlled- or sustained-release formulations of a pharmaceutical composition of the invention can be made using conventional technology.

A formulation of a pharmaceutical composition of the invention suitable for oral administration can be prepared, packaged, or sold in the form of a discrete solid dose unit including, but not limited to, a tablet, a hard or soft capsule, a cachet, a troche, or a lozenge, each containing a predetermined amount of the active ingredient. Other formulations suitable for oral administration include, but are not limited to, a powdered or granular formulation, an aqueous or oily suspension, an aqueous or oily solution, or an emulsion.

As used herein, an "oily" liquid is one which comprises a carbon-containing liquid molecule and which exhibits a less polar character than water.

A tablet comprising the active ingredient may, for example, be made by compressing or molding the active ingredient, optionally with one or more additional ingredients. Compressed tablets can be prepared by compressing, in a suitable device, the active ingredient in a free-flowing form such as a powder or granular preparation, optionally mixed with one or more of a binder, a lubricant, an excipient, a surface active agent, and a dispersing agent. Molded tablets can be made by molding, in a suitable device, a mixture of the active ingredient, a pharmaceutically acceptable carrier, and at least sufficient liquid to moisten the mixture. Pharmaceutically acceptable excipients used in the manufacture of tablets include, but are not limited to, inert diluents, granulating and disintegrating agents, binding agents, and lubricating

agents. Known dispersing agents include, but are not limited to, potato starch and sodium starch glycolate. Known surface active agents include, but are not limited to, sodium lauryl sulfate. Known diluents include, but are not limited to, calcium carbonate, sodium carbonate, lactose, microcrystalline cellulose, calcium phosphate, calcium hydrogen phosphate, and sodium phosphate. Known granulating and disintegrating agents include, but are not limited to, corn starch and alginic acid. Known binding agents include, but are not limited to, gelatin, acacia, pre-gelatinized maize starch, polyvinylpyrrolidone, and hydroxypropyl methylcellulose. Known lubricating agents include, but are not limited to, magnesium stearate, stearic acid, silica, and talc.

Tablets can be non-coated or they can be coated using known methods to achieve delayed disintegration in the gastrointestinal tract of a subject, thereby providing sustained release and absorption of the active ingredient. By way of example, a material such as glyceryl monostearate or glyceryl distearate can be used to coat tablets. Further by way of example, tablets can be coated using methods described in U.S. Patents numbers 4,256,108; 4,160,452; and 4,265,874 to form osmotically-controlled release tablets. Tablets can further comprise a sweetening agent, a flavoring agent, a coloring agent, a preservative, or some combination of these in order to provide pharmaceutically elegant and palatable preparation.

Hard capsules comprising the active ingredient can be made using a physiologically degradable composition, such as gelatin. Such hard capsules comprise the active ingredient, and can further comprise additional ingredients including, for example, an inert solid diluent such as calcium carbonate, calcium phosphate, or kaolin.

Soft gelatin capsules comprising the active ingredient can be made using a physiologically degradable composition, such as gelatin. Such soft capsules comprise the active ingredient, which can be mixed with water or an oil medium such as peanut oil, liquid paraffin, or olive oil.

Liquid formulations of a pharmaceutical composition of the invention which are suitable for oral administration can be prepared, packaged, and sold either in liquid form or in the form of a dry product intended for reconstitution with water or another suitable vehicle prior to use.

Liquid suspensions can be prepared using conventional methods to achieve suspension of the active ingredient in an aqueous or oily vehicle. Aqueous vehicles include, for example, water and isotonic saline. Oily vehicles include, for example, almond oil, oily esters, ethyl alcohol, vegetable oils such as arachis, olive, sesame, or coconut oil, fractionated vegetable oils, and mineral oils such as liquid paraffin. Liquid suspensions can further comprise one or more additional ingredients including, but not limited to, suspending agents, dispersing or wetting agents, emulsifying agents, demulcents, preservatives, buffers, salts, flavorings, coloring agents, and sweetening agents. Oily suspensions can further comprise a thickening agent. Known suspending agents include, but are not limited to, sorbitol syrup, hydrogenated edible fats, sodium alginate, polyvinylpyrrolidone, gum tragacanth, gum acacia, and cellulose derivatives such as sodium carboxymethylcellulose, methylcellulose, hydroxypropylmethylcellulose. Known dispersing or wetting agents include, but are not limited to, naturally-occurring phosphatides such as lecithin, condensation products of an alkylene oxide with a fatty acid, with a long chain aliphatic alcohol, with a partial ester derived from a fatty acid and a hexitol, or with a partial ester derived from a fatty acid and a hexitol anhydride (e.g. polyoxyethylene stearate, heptadecaethyleneoxycetanol, polyoxyethylene sorbitol monooleate, and polyoxyethylene sorbitan monooleate, respectively). Known emulsifying agents include, but are not limited to, lecithin and acacia. Known preservatives include, but are not limited to, methyl, ethyl, or n-propyl-para- hydroxybenzoates, ascorbic acid, and sorbic acid. Known sweetening agents include, for example, glycerol, propylene glycol, sorbitol, sucrose, and saccharin. Known thickening agents for oily suspensions include, for example, beeswax, hard paraffin, and cetyl alcohol.

Liquid solutions of the active ingredient in aqueous or oily solvents can be prepared in substantially the same manner as liquid suspensions, the primary difference being that the active ingredient is dissolved, rather than suspended in the solvent. Liquid solutions of the pharmaceutical composition of the invention can comprise each of the components described with regard to liquid suspensions, it being understood that suspending agents will not necessarily aid dissolution of the active ingredient in the solvent. Aqueous solvents include, for example, water and isotonic saline. Oily solvents include, for example, almond oil, oily esters, ethyl alcohol, vegetable oils such as arachis, olive, sesame, or coconut oil, fractionated vegetable oils, and mineral oils such as liquid paraffin.

Powdered and granular formulations of a pharmaceutical preparation of the invention can be prepared using known methods. Such formulations can be administered directly to a subject, used, for example, to form tablets, to fill capsules, or to prepare an aqueous or oily suspension or solution by addition of an aqueous or oily vehicle thereto. Each of these formulations can further comprise one or more of dispersing or wetting agent, a suspending agent, and a preservative. Additional excipients, such as fillers and sweetening, flavoring, or coloring agents, can also be included in these formulations.

A pharmaceutical composition of the invention can also be prepared, packaged, or sold in the form of oil-in-water emulsion or a water-in-oil emulsion. The oily phase can be a vegetable oil such as olive or arachis oil, a mineral oil such as liquid paraffin, or a combination of these. Such compositions can further comprise one or more emulsifying agents such as naturally occurring gums such as gum acacia or gum tragacanth, naturally-occurring phosphatides such as soybean or lecithin phosphatide, esters or partial esters derived from combinations of fatty acids and hexitol anhydrides such as sorbitan monooleate, and condensation products of such partial esters with ethylene oxide such as polyoxyethylene sorbitan monooleate. These emulsions can also contain additional ingredients including, for example, sweetening or flavoring agents.

A pharmaceutical composition of the invention can be prepared, packaged, or sold in a formulation suitable for rectal administration. Such a composition can be in the form of, for example, a suppository, a retention enema preparation, and a solution for rectal or colonic irrigation.

Suppository formulations can be made by combining the active ingredient with a non-irritating pharmaceutically acceptable excipient which is solid at ordinary room temperature (i.e. about 20°C) and which is liquid at the rectal temperature of the subject (i.e. about 37°C in a healthy human). Suitable pharmaceutically acceptable excipients include, but are not limited to, cocoa butter, polyethylene glycols, and various glycerides. Suppository formulations can further comprise various additional ingredients including, but not limited to, antioxidants and preservatives.

Retention enema preparations or solutions for rectal or colonic irrigation can be made by combining the active ingredient with a pharmaceutically acceptable liquid carrier. As is well known in the art, enema preparations can be administered using, and can be packaged within, a delivery device adapted to the rectal anatomy of the subject. Enema preparations can further comprise various additional ingredients including, but not limited to, antioxidants and preservatives.

A pharmaceutical composition of the invention can be prepared, packaged, or sold in a formulation suitable for vaginal administration. Such a composition can be in the form of, for example, a suppository, an impregnated or coated vaginally-insertable material such as a tampon, a douche preparation, or a solution for vaginal irrigation.

Methods for impregnating or coating a material with a chemical composition are known in the art, and include, but are not limited to methods of depositing or binding a chemical composition onto a surface, methods of incorporating a chemical composition into the structure of a material during the synthesis of the material (i.e. such as with a physiologically degradable material), and methods of

absorbing an aqueous or oily solution or suspension into an absorbent material, with or without subsequent drying.

Douche preparations or solutions for vaginal irrigation can be made by combining the active ingredient with a pharmaceutically acceptable liquid carrier. As is well known in the art, douche preparations can be administered using, and can be packaged within, a delivery device adapted to the vaginal anatomy of the subject. Douche preparations can further comprise various additional ingredients including, but not limited to, antioxidants, antibiotics, antifungal agents, and preservatives.

As used herein, "parenteral administration" of a pharmaceutical composition includes any route of administration characterized by physical breaching of a tissue of a subject and administration of the pharmaceutical composition through the breach in the tissue. Parenteral administration thus includes, but is not limited to, administration of a pharmaceutical composition by injection of the composition, by application of the composition through a surgical incision, by application of the composition through a tissue-penetrating non-surgical wound, and the like. In particular, parenteral administration is contemplated to include, but is not limited to, subcutaneous, intraperitoneal, intravenous, intraarterial, intramuscular, or intrasternal injection and intravenous, intraarterial, or kidney dialytic infusion techniques.

Formulations of a pharmaceutical composition suitable for parenteral administration comprise the active ingredient combined with a pharmaceutically acceptable carrier, such as sterile water or sterile isotonic saline. Such formulations can be prepared, packaged, or sold in a form suitable for bolus administration or for continuous administration. Injectable formulations can be prepared, packaged, or sold in unit dosage form, such as in ampules or in multi-dose containers containing a preservative. Formulations for parenteral administration include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-release or biodegradable formulations. Such formulations can further comprise one or more additional ingredients including, but not limited to, suspending, stabilizing, or dispersing agents. In one embodiment of a formulation for parenteral

administration, the active ingredient is provided in dry (i.e. powder or granular) form for reconstitution with a suitable vehicle (e.g. sterile pyrogen-free water) prior to parenteral administration of the reconstituted composition.

The pharmaceutical compositions can be prepared, packaged, or sold in the form of a sterile injectable aqueous or oily suspension or solution. This suspension or solution can be formulated according to the known art, and can comprise, in addition to the active ingredient, additional ingredients such as the dispersing agents, wetting agents, or suspending agents described herein. Such sterile injectable formulations can be prepared using a non-toxic parenterally-acceptable diluent or solvent, such as water or 1,3-butane diol, for example. Other acceptable diluents and solvents include, but are not limited to, Ringer's solution, isotonic sodium chloride solution, and fixed oils such as synthetic mono- or di-glycerides. Other parentally-administrable formulations which are useful include those which comprise the active ingredient in microcrystalline form, in a liposomal preparation, or as a component of a biodegradable polymer systems. Compositions for sustained release or implantation can comprise pharmaceutically acceptable polymeric or hydrophobic materials such as an emulsion, an ion exchange resin, a sparingly soluble polymer, or a sparingly soluble salt.

Formulations suitable for topical administration include, but are not limited to, liquid or semi-liquid preparations such as liniments, lotions, oil-in-water or water-in-oil emulsions such as creams, ointments or pastes, and solutions or suspensions. Topically-administrable formulations may, for example, comprise from about 1% to about 10% (w/w) active ingredient, although the concentration of the active ingredient can be as high as the solubility limit of the active ingredient in the solvent. Formulations for topical administration can further comprise one or more of the additional ingredients described herein.

A pharmaceutical composition of the invention can be prepared, packaged, or sold in a formulation suitable for pulmonary administration via the buccal cavity. Such a formulation can comprise dry particles which comprise the active ingredient and which have a diameter in the range from about 0.5 to about 7

nanometers, and preferably from about 1 to about 6 nanometers. Such compositions are conveniently in the form of dry powders for administration using a device comprising a dry powder reservoir to which a stream of propellant can be directed to disperse the powder or using a self-propelling solvent/powder-dispensing container such as a device comprising the active ingredient dissolved or suspended in a low-boiling propellant in a sealed container. Preferably, such powders comprise particles wherein at least 98% of the particles by weight have a diameter greater than 0.5 nanometers and at least 95% of the particles by number have a diameter less than 7 nanometers. More preferably, at least 95% of the particles by weight have a diameter greater than 1 nanometer and at least 90% of the particles by number have a diameter less than 6 nanometers. Dry powder compositions preferably include a solid fine powder diluent such as sugar and are conveniently provided in a unit dose form.

Low boiling propellants generally include liquid propellants having a boiling point of below 65°F at atmospheric pressure. Generally the propellant can constitute 50 to 99.9% (w/w) of the composition, and the active ingredient can constitute 0.1 to 20% (w/w) of the composition. The propellant can further comprise additional ingredients such as a liquid non-ionic or solid anionic surfactant or a solid diluent (preferably having a particle size of the same order as particles comprising the active ingredient).

Pharmaceutical compositions of the invention formulated for pulmonary delivery can also provide the active ingredient in the form of droplets of a solution or suspension. Such formulations can be prepared, packaged, or sold as aqueous or dilute alcoholic solutions or suspensions, optionally sterile, comprising the active ingredient, and can conveniently be administered using any nebulization or atomization device. Such formulations can further comprise one or more additional ingredients including, but not limited to, a flavoring agent such as saccharin sodium, a volatile oil, a buffering agent, a surface active agent, or a preservative such as methylhydroxybenzoate. The droplets provided by this route of administration preferably have an average diameter in the range from about 0.1 to about 200 nanometers.

The formulations described herein as being useful for pulmonary delivery are also useful for intranasal delivery of a pharmaceutical composition of the invention.

Another formulation suitable for intranasal administration is a coarse powder comprising the active ingredient and having an average particle from about 0.2 to 500 micrometers. Such a formulation is administered in the manner in which snuff is taken i.e. by rapid inhalation through the nasal passage from a container of the powder held close to the nares.

Formulations suitable for nasal administration may, for example, comprise from about as little as 0.1% (w/w) and as much as 100% (w/w) of the active ingredient, and can further comprise one or more of the additional ingredients described herein.

A pharmaceutical composition of the invention can be prepared, packaged, or sold in a formulation suitable for buccal administration. Such formulations may, for example, be in the form of tablets or lozenges made using conventional methods, and may, for example, 0.1 to 20% (w/w) active ingredient, the balance comprising an orally dissolvable or degradable composition and, optionally, one or more of the additional ingredients described herein. Alternately, formulations suitable for buccal administration can comprise a powder or an aerosolized or atomized solution or suspension comprising the active ingredient. Such powdered, aerosolized, or aerosolized formulations, when dispersed, preferably have an average particle or droplet size in the range from about 0.1 to about 200 nanometers, and can further comprise one or more of the additional ingredients described herein.

A pharmaceutical composition of the invention can be prepared, packaged, or sold in a formulation suitable for ophthalmic administration. Such formulations may, for example, be in the form of eye drops including, for example, a 0.1-1.0% (w/w) solution or suspension of the active ingredient in an aqueous or oily liquid carrier. Such drops can further comprise buffering agents, salts, or one or more other of the additional ingredients described herein. Other ophthalmalmically-

administrable formulations which are useful include those which comprise the active ingredient in microcrystalline form or in a liposomal preparation.

As used herein, "additional ingredients" include, but are not limited to, one or more of the following: excipients; surface active agents; dispersing agents; inert diluents; granulating and disintegrating agents; binding agents; lubricating agents; sweetening agents; flavoring agents; coloring agents; preservatives; physiologically degradable compositions such as gelatin; aqueous vehicles and solvents; oily vehicles and solvents; suspending agents; dispersing or wetting agents; emulsifying agents, demulcents; buffers; salts; thickening agents; fillers; emulsifying agents; antioxidants; antibiotics; antifungal agents; stabilizing agents; and pharmaceutically acceptable polymeric or hydrophobic materials. Other "additional ingredients" which can be included in the pharmaceutical compositions of the invention are known in the art and described, for example in Genaro, ed., 1985, Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, PA, which is incorporated herein by reference.

A pharmaceutical composition of the invention can be prepared, packaged, or sold in bulk, as a single unit dose, or as a plurality of single unit doses. As used herein, a "unit dose" is discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

The relative amounts of the active ingredient, the pharmaceutically acceptable carrier, and any additional ingredients in a pharmaceutical composition of the invention will vary, depending upon the identity, size, and condition of the subject treated and further depending upon the route by which the composition is to be administered. By way of example, the composition can comprise between 0.1% and 100% (w/w) active ingredient. A unit dose of a pharmaceutical composition of the invention will depend upon the type of active ingredient contained therein. Generally, pharmaceutical compositions which comprise an expression vector should be

administered in an amount sufficient to provide at least one expression vector to the cell(s) being treated. It is understood that the precise dosage of the vector will depend upon the efficiency with which the vector enters and transforms target cells, the number of such cells to be treated, the physical accessibility of the cells to the vector, and other factors which will be understood by the skilled in light of the present disclosure. Pharmaceutical compositions comprising an expression vector are preferably administered in an amount sufficient to provide a two-, five-, ten-, or fifty-fold excess, or more, of the minimum recommended amount of the vector to individual cells. Pharmaceutical compositions comprising an ASO should be administered in an amount sufficient to provide at least a quantity of ASO molecules equal to at least the expected or determined number of genomic copies of the ASO target or transcripts thereof. Pharmaceutical compositions comprising an ASO are preferably administered in an amount sufficient to provide a two-, ten-, one hundred-, or one thousand-fold excess, or more, of the minimum recommended amount of the ASO to the target cells.

It is understood that the ordinarily skilled physician or veterinarian will readily determine and prescribe an effective amount of the active ingredient(s) for performing the methods of the invention in a subject. In so proceeding, the physician or veterinarian may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. It is further understood, however, that the specific dose level for any particular subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the severity of the condition being treated.

Another aspect of the invention relates to a kit comprising a pharmaceutical composition of the invention and an instructional material. The instructional material of the kit of the invention may, for example, be affixed to a container which contains a pharmaceutical composition of the invention or be shipped together with a container which contains the pharmaceutical composition.

Alternatively, the instructional material can be shipped separately from the container with the intention that the instructional material and the pharmaceutical composition be used cooperatively by the recipient.

The invention also includes a kit comprising a pharmaceutical composition of the invention and a delivery device for delivering the composition to a subject. By way of example, the delivery device can be a squeezable spray bottle, a metered-dose spray bottle, an aerosol spray device, an atomizer, a dry powder delivery device, a self-propelling solvent/powder-dispensing device, a syringe, a needle, a tampon, or a dosage measuring container. The kit can further comprise an instructional material as described herein.

Screening Methods of the Invention

Identification of the human *FEZ1* gene as a tumor suppressor gene, as described herein, provides a means for identifying compounds which induce cell proliferation. Also, because some altered *FEZ1* genes associated with cancers in humans can prove to be capable of expression at normal, or near normal, levels in the presence of certain compounds, a method is provided for identifying such compounds, which can inhibit abnormal cell proliferation in cells having an altered *FEZ1* gene, such as tumor cells and tissues.

The invention therefore includes a method of determining whether a test compound is an inducer of cell proliferation. This method comprises incubating a cell which comprises a functional *FEZ1* gene in the presence of the test compound and assessing expression of *FEZ1* in the cell. If expression of *FEZ1* in the cell is decreased relative to expression of *FEZ1* in a cell of the same type incubated in the absence of the test compound, then the test compound is an inducer of cell proliferation. Particularly contemplated test compounds include isolated polynucleotides of the invention, as described herein. This method is therefore a useful way to identify ASOs which inhibit expression of *FEZ1* and which therefore induce cell proliferation.

The cell which is used in this method can be substantially any cell which expresses a *FEZ1* gene, such as one which transcribes the *FEZ1* gene or one

which both transcribes and translates *FEZ1*. Preferably, the cell is a human cell, and it is more preferably an epithelial cell. When identification of a compound which induces proliferation of a certain cell type is desired, it is preferred that the cell used in this screening method be a cell of that certain type.

Expression of *FEZ1* in the cell can be assessed by any known method of assessing gene expression. For example, the accumulated or steady-state amount of a transcript of *FEZ1* or the rate of production of such a transcript in the cell of the screening method can be assessed using known methods. Alternately, the accumulated or steady-state amount of Fez1 protein or the rate of production of Fez1 protein can be assessed, likewise using known methods, including immunological methods involving an antibody of the invention.

The test compound can be administered to the cell in substantially any way. Preferably, the cell is incubated in a medium comprising the test compound. Where the test compound does not readily pass from the medium to the interior of the cell (e.g. the test compound is a protein or a large nucleic acid in a form which does not normally cross cell membranes) a vector can be used to deliver the test compound to the interior of the cell. However, because the screening method is intended to identify compounds which can be administered to a cell in the most convenient and physiologically acceptable form possible, it is preferred that the test compound not require a vector in order to reach the interior of the cell. Of course, it is understood that if no effective test compounds can be identified which do not require a vector in order to gain cell entry, it can be advantageous to assess the effectiveness of vector-borne test compounds.

It is not necessary that expression of *FEZ1* be assessed in a cell of the same type every time a test compound is assayed. Instead, a body of data can be developed which relate to the level of *FEZ1* expression in such a cell under the conditions used to assay the test compound.

The invention also relates to a method of determining whether a test compound is effective to retard proliferation of a cell having an altered *FEZ1* gene.

This method comprises incubating the cell having an altered *FEZ1* gene in the presence of the test compound and assessing expression of *FEZ1* in the cell. If expression of *FEZ1* in the cell is increased, relative to expression of *FEZ1* in a cell of the same type (i.e. also having the same altered *FEZ1* gene) incubated in the absence of the test compound, then the test compound is effective to retard proliferation of a cell. This result furthermore indicates that the test compound is a useful cancer therapeutic compound for treating cancer in a tissue which comprises cells of the type used in this screening assay. This screening method is performed in substantially the same manner as the screening method described in the preceding paragraphs, except that the cell used in the screening method has an altered *FEZ1* gene.

The presence of a leucine-zipper-like region in the putative amino acid sequence of Fez1 protein, as described herein, suggests that Fez1 protein is a nucleic acid-binding protein. This information indicates that it is possible to identify at least one nucleic acid sequence with which Fez1 protein binds by contacting Fez1 protein with a test nucleic acid sequence and assessing whether the protein and the nucleic acid form a complex. Any known method for detecting such complexes can be used, including, but not limited to, nucleic acid footprint methods, altered gel electrophoresis mobility methods, altered chromatographic mobility methods, immunological methods involving an antibody of the invention. Once such a sequence has been identified, a nucleic acid comprising that sequence can be used as an inducer of cell proliferation by delivering such a nucleic acid to a cell comprising a functional Fez1 protein. The nucleic acid binds with the Fez1 protein in the cell, preventing Fez1 from binding with its normal physiological binding partner, and thereby inducing cell proliferation. In such a method, the nucleic acid is preferably used in great excess (e.g. 10-, 100-, or 1000-fold or more excess) of the intracellular concentration of Fez1 protein.

The screening methods of the invention can be used to identify anti-cancer therapeutic compounds for administration to a human afflicted with a cancer by identifying test compounds a inducers of altered *FEZ1* gene expression. Because the human *FEZ1* gene can be altered in numerous ways in various cancers and in different

individuals, it is advantageous to perform the screening methods of the invention using cells obtained from the patient to be treated. In order to facilitate such treatment, components used in these assay methods can be conveniently packaged in the form of a kit comprising a plurality of candidate anti-cancer therapeutic compounds and a reagent for assessing expression of *FEZ1* in the patient's cells. In one embodiment, the reagent is an isolated polynucleotide which anneals with high stringency with a human *FEZ1* gene, such as an isolated polynucleotide which anneals with high stringency with at least twenty consecutive nucleotide residues of at least one strand of SEQ ID NO: 1. In another embodiment, the reagent is the antibody of the invention, as described herein.

The invention includes a screening method for determining whether a test compound is useful for alleviating a disorder associated with aberrant tubulin polymerization. This method comprising comparing

(i) tubulin polymerization in a first assay mixture which comprises tubulin, Fez1, and the test compound and

(ii) tubulin polymerization in a second assay mixture which comprises tubulin and Fez1, but which does not comprise the test compound.

A difference (e.g. a difference between the rate of tubulin polymerization in the first and second assay mixtures or a difference between the extent of tubulin polymerization in the first and second assay mixtures between tubulin polymerization in the first and second assay mixtures) is an indication that the test compound is useful for alleviating the disorder. Preferably, the first and second assay mixtures are substantially identical, but for the presence or absence of the test compound.

Disorders which can test compounds can be tested include both tubulin hyperpolymerization disorders and tubulin hypopolymerization disorders. For example, the disorder can be one selected from the group consisting of a disorder associated with aberrant initiation of mitosis, a disorder associated with aberrant modulation of the rate and stage of mitosis, a disorder associated with aberrant modulation of the initiation and rate of cell proliferation, a disorder associated with aberrant modulation of the initiation and rate of cell growth, a disorder associated with

aberrant modulation of cell shape, a disorder associated with aberrant modulation of cell rigidity, a disorder associated with aberrant modulation of cell motility, a disorder associated with aberrant modulation of the rate of cellular DNA replication, a disorder associated with aberrant modulation of the stage of cellular DNA replication, a disorder associated with aberrant modulation of the intracellular distribution of organelles, a disorder associated with aberrant modulating the metastatic potential of a cell, and a disorder associated with aberrant modulation of cellular transformation from a non-cancerous to a cancerous phenotype. Particular examples of such disorders include tumorigenesis, tumor survival, tumor growth, and tumor metastasis.

The test compound used in this screening method can be substantially any compound. Compounds which are anticipated to be particularly likely to be useful for alleviating such disorders include ones selected from the group consisting of a fragment of Fez1, a peptidomimetic of a fragment of Fez1, a fragment of tubulin, a peptidomimetic of a fragment of tubulin, a fragment of EF1-γ, and a peptidomimetic of a fragment of EF1-γ.

The invention includes another screening method for determining whether a test compound is useful for alleviating a disorder associated with aberrant phosphorylation of Fez1. This method comprises comparing

(i) phosphorylation of Fez1 in a first assay mixture which comprises Fez1, at least one kinase, a phosphate source, and the test compound and

(ii) phosphorylation of Fez1 in a second assay mixture which comprises Fez1, the kinase, and the phosphate source, but which does not comprise the test compound. A difference between phosphorylation of Fez1 in the first and second assay mixtures (e.g. a difference in the rate or degree of phosphorylation in the first and second assay mixtures) is an indication that the test compound is useful for alleviating the disorder. This screening method can be used to assess the utility of compounds for alleviating the same disorders referred to above.

The invention includes yet another screening method for determining whether a test compound is useful for alleviating a disorder associated with aberrant phosphorylation of Fez1. This method comprising comparing

(i) phosphorylation of Fez1 in a first assay mixture which comprises phosphorylated Fez1, at least one phosphatase, and the test compound and

(ii) phosphorylation of Fez1 in a second assay mixture which comprises phosphorylated Fez1 and the phosphatase, but which does not comprise the test compound.

A difference between phosphorylation of Fez1 in the first and second assay mixtures (e.g. a difference in the rate or extent of de-phosphorylation of phosphorylated Fez1) is an indication that the test compound is useful for alleviating the disorder. This screening method can be used to assess the utility of compounds for alleviating the same disorders referred to above.

The invention also includes a method of determining whether a test compound is useful for alleviating a disorder associated with aberrant binding of Fez1 with a protein with which Fez1 normally binds, the method comprising comparing

(i) binding between Fez1 and the protein in a first assay mixture which comprises Fez1, the protein, and the test compound and

(ii) binding between Fez1 and the protein in a second assay mixture which comprises Fez1 and the protein, but which does not comprise the test compound.

A difference between (e.g. the rate or degree of) binding of Fez1 and the protein in the first and second assay mixtures is an indication that the test compound is useful for alleviating the disorder. The protein can, for example, be selected from the group consisting of tubulin and EF1-γ. This screening method is useful for assessing the utility of a test compound for alleviating a disorders such as one of tumorigenesis, tumor survival, tumor growth, and tumor metastasis.

The invention includes a method of determining whether a test compound is an inhibitor of cell proliferation. This method comprises incubating a cell which comprises a functional *FEZ1* gene in the presence of the test compound and

assessing expression of *FEZ1* in the cell. If expression of *FEZ1* in the cell is increased, relative to expression of *FEZ1* in a cell of the same type incubated in the absence of the test compound, then this is an indication that the test compound is an inhibitor of cell proliferation.

Cell Proliferation Methods of the Invention

As described herein, the human *FEZ1* gene has been discovered to be a tumor suppressor gene. Thus, inactivation of this gene, or inhibition of expression of this gene, leads to the enhanced rate of cell proliferation associated with cancer. In certain situations, however, enhanced cell proliferation is desirable. For example, some *in vitro* cell culture methods are limited by the rate of cell proliferation and by effects of cell density on this rate. Further by way of example, in certain medical procedures, such as in bone marrow transplants and skin allografts, it is desirable that cells proliferate at a greater-than-normal rate for a period and subsequently proliferate only at a normal rate. These methods would be enhanced if cell proliferation could be enhanced, especially if it could be enhanced in a reversible manner.

Providing a cell with an inhibitor of *FEZ1* expression enhances the rate of proliferation of the cell, and this technique can be used to improve a variety of known methods in which the rate of cell proliferation was a limiting factor. For example, by including an inhibitor of *FEZ1* expression in a cell culture medium, or by treating cells (e.g. human epithelial cells) growing on or in such medium with such an inhibitor, the *in vitro* rate of cell proliferation can be increased, permitting faster and denser cell growth than would otherwise be possible.

Similarly, by treating human cells, especially epithelial cells, *in vivo* with an inhibitor of *FEZ1* expression, the rate of proliferation of those cells can be increased. This method can be used, for example to enhance graft integration into the graft site or to improve reestablishment of bone marrow in an individual who has been subjected to levels of radiation or cytotoxic chemicals that are sufficient to cause bone marrow loss. Local administration of the inhibitor to the tissue(s) or region(s) in which

enhanced cell proliferation is desired minimizes undesirable cell proliferation in other tissues and at other body regions. Discontinuing administration of the inhibitor leads eventually to normal cell proliferation of treated cells, owing to degradation of the inhibitor.

Likewise, cells obtained from a human can be treated *ex vivo* with an inhibitor of *FEZ1* expression to enhance their rate of proliferation prior to implanting those cells within the same human from which they were obtained or within a different human. The same or a different inhibitor of *FEZ1* expression can be administered, locally or systemically, to the human cell recipient in order to maintain the enhanced rate of proliferation of the treated cells, or the cells can instead be permitted to retain their enhanced rate of proliferation only so long as the inhibitor delivered to them *ex vivo* endures. In either event, the *ex vivo* treated cells assume a normal rate of proliferation after the inhibitor(s) are degraded and not replaced.

In the cell proliferation enhancement methods described herein, the inhibitor of *FEZ1* expression can optionally be a molecule which is capable of being replicated in a human cell, such as a virus vector encoding such an inhibitor, for example. Where it is considered desirable to be able to reversibly induce enhanced cell proliferation, the inhibitor is preferably not capable of being replicated in a human cell. Furthermore, in some embodiments, it is preferable that the inhibitor be provided to the cells in the form of a vector which comprises a polynucleotide encoding the inhibitor, and that the polynucleotide be operably linked to an inducible promoter, so that production of the inhibitor can be initiated and concluded by administration and withholding, respectively, of the inducer of the promoter.

Kits of the Invention

The invention includes various kits which comprise any two or more of the isolated polynucleotides of the invention, the isolated Fez1 proteins of the invention, pharmaceutical compositions, and instructional materials which describe use of these polynucleotides and proteins to perform the diagnostic, therapeutic, or screening methods of the invention. Although exemplary kits are described below, the

contents of other useful kits will be apparent to the skilled artisan in light of the present disclosure. Each of these kits is included within the invention.

An example of a kit of the invention is a kit for amplifying at least a portion of a human *FEZ1* gene. This kit comprising a first isolated polynucleotide and a second isolated polynucleotide, wherein the first isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of one strand of a human *FEZ1* gene and the second isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the other strand of the gene. For example, the first isolated polynucleotide can be one which anneals with high stringency with at least twenty consecutive nucleotide residues of the coding strand of SEQ ID NO: 1, and the second isolated polynucleotide can be one which anneals with high stringency with at least twenty consecutive nucleotide residues of the non-coding strand of SEQ ID NO: 1. This kit can further comprise other components of a reaction mixture for amplifying a region of a nucleic acid, such as a DNA polymerase (e.g. *Thermus aquaticus* DNA polymerase) or deoxyribonucleotides. Alternately, or in addition, this kit can include an instructional material which describes the polynucleotides as being useful for amplifying a portion of the gene or which describe how to perform such an amplification.

A second example of a kit of the invention is a kit for amplifying at least a portion of a cDNA generated from a transcript of a human *FEZ1* gene. This kit comprises a first isolated polynucleotide and a second isolated polynucleotide. The first isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the cDNA, and the second isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the cDNA. In one embodiment of this kit, the first isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the coding strand of SEQ ID NO: 1, and the second isolated polynucleotide anneals with high stringency with at least twenty consecutive nucleotide residues of the non-coding strand of SEQ ID NO: 1.

The invention is now described with reference to the following Examples. These Examples are provided for the purpose of illustration only and the invention is not limited to these Examples, but rather encompass all variations which are evident as a result of the teaching provided herein.

Example 1

The *FEZ1* Gene at Chromosome Location 8p22 Encodes a Leucine-Zipper Protein, and its Expression Is Altered in Multiple Human Tumors

Loss of heterozygosity (LOH) at 8p22 is a common characteristic of epithelial tumors, including breast, prostate, and esophageal carcinomas. In the experiments presented in this Example, altered expression and mutations of the *FEZ1* gene at 8p22 were demonstrated in numerous cancer cell lines and tumor samples, thereby demonstrating that the *FEZ1* gene is at least one of the tumor suppressor genes which had previously been hypothesized to be located near 8p21-22.

As described herein for the first time, *FEZ1* encodes a leucine-zipper protein having substantial amino acid sequence similarity to the DNA-binding protein designated Atf-5. *FEZ1* expression could not be detected in more than 60% of epithelial tumors and tumor cell lines of various types. Furthermore, transcript analysis of *FEZ1*-expressing tumor cells indicated the presence of mutations in *FEZ1*, as evidenced by the presence of sequence abnormalities in the *FEZ1* transcript, and the presence of frame-shift mutations, as evidenced by the presence of truncated *FEZ1* transcripts. Based on the results described in this Example, it is concluded that alteration or inactivation of *FEZ1* is involved in development of multiple human tumors, including epithelial tumors.

The materials and methods used in the experiments presented in this Example are now described.

Esophageal cancer cell lines were cultured in RPMI 1640 medium supplemented with 10% (v/v) fetal bovine serum. Prostate cancer cell lines, breast cancer cell lines, hematological cell lines, and HeLa cells were obtained from the American Type Culture Collection and were cultured as described (Negrini, 1996).

Tumor and non-tumor tissue samples were obtained from 72 patients afflicted with primary esophageal cancers, 39 patients afflicted with breast cancers, 24 patients afflicted with prostate cancers, and 8 patients afflicted with ovarian cancers.

Chromosomal DNA was isolated from 53 primary esophageal squamous cell tumors and from matched normal tissue samples obtained from the same patients. These DNA samples were analyzed for allele loss at 22 microsatellite loci on chromosome 8p.

PCR amplification of microsatellite loci using FAM- or TET-labeled primers (Research Genetics, Huntsville, AL) were performed as described (Niederacher et al., 1997, Genes Chromosom. Cancer 18:181), with minor modifications. Briefly, PCR was performed using AmpliTaq™ Gold (Perkin Elmer Cetus, Norwalk, CT), using the following reaction conditions. After heating the reaction mixture to 95°C for 12 minutes, a total of 30 PCR cycles were performed. The first 10 cycles consisted of maintaining the reaction mixture at 94°C for 15 seconds, at 55-58°C for 15 seconds (to anneal DNA strands), and at 72°C for 30 seconds. The next 20 cycles consisted of maintaining the reaction mixture at 89°C for 15 seconds, at 55-58°C for 15 seconds (to anneal DNA strands), and at 72°C for 30 seconds. Following these 30 cycles, the reaction mixture was maintained at 72°C for 30 minutes. Following heat denaturation, the amplified reaction mixtures were loaded on a 6% (w/v)polyacrylamide denaturing gel on the Applied Biosystems model 373 DNA sequencer. Data collection and fragment analysis were performed using ABI Prism™ Genescan and ABI Prism™ Genotyper Analysis Software (Perkin Elmer Cetus, Norwalk, CT; Applied Biosystems, Inc., Foster City, CA).

LOH was detected as reduction by more than 50% of an allele peak signal in DNA obtained from a tumor sample, relative to the peak signal of the same allele in corresponding normal tissue. If a tumor sample demonstrated 40-60% reduction of an allele peak signal, relative to the corresponding normal tissue, the analyses were repeated two more times, and average reductions were used as final data.

Yeast artificial chromosome (YAC) and bacterial artificial chromosome (BAC) contigs of the region of the genome near the *D8S261* marker were constructed. The relative positions of the YAC and BAC contigs, relative to certain microsatellite loci, are indicated in Figure 1C.

Human chromosome 8p BAC DNA samples were sequenced using primers T7 and SP6 (Research Genetics, Huntsville, AL). Southern blot hybridization and PCR analysis indicated that BAC clones overlapped, and contigs were constructed.

PCR amplification was performed using STS (sequence tagged sequences) primers in order to screen a human YAC library obtained from Research Genetics (Huntsville, AL). A mixture of YAC clones was embedded in an agarose gel and separated by pulse-field gel electrophoresis (PFGE), as described (Ausubel et al., 1989, In: Current Protocols in Molecular Biology, Wiley-Interscience, New York; Bookstein, et al., 1994, Genomics 24:317). Following PFGE, YAC DNA was transferred to a nylon membrane in the presence of 0.4 molar sodium hydroxide, and the membrane was hybridized using human genomic DNA. DNA from individual YAC clones was digested within the gel using *MboI* for four hours at 37°C. Digested YAC clone DNA was extracted from the gel using a Gene Clean III™ kit obtained from BIO 101, Inc. (La Jolla, CA), per the kit instructions.

In order to clone the genes present in YAC clone DNA, two deoxy-oligonucleotides, 5'-GATCTCGACG AATTCGTGAG ACCT-3' (SEQ ID NO: 44) and 5'-TGGTCTCACG AATTCGTCGA-3' (SEQ ID NO: 45), were annealed to form a partially-double stranded adapter-linker. This adapter-linker was ligated to the digested YAC clone DNA. Fifteen cycles of PCR amplifications were performed using 5'-biotinylated primers corresponding to the adapter-linker. PCR products were sequenced and confirmed not to be yeast genomic DNA.

cDNAs were synthesized by reverse transcription of prostate poly(A)$^+$ RNA using *NotI*-primer adaptor/oligo-dT primers according to the GC rich protocol (Superscript™ Plasmid system; Gibco-BRL, Grand Island, NY). A Sal I adaptor

(Gibco-BRL, Grand Island, NY) was ligated to the cDNAs, and those cDNAs were subjected to twenty cycles of PCR amplification using adapter primers.

Blocking, hybridizing, and washing methods were adapted from described procedures (Bookstein et al., 1997, Br. J. Urol. 79(Suppl. 1):28; Bova et al., 1996, Genomics 35:46; MacGrogan et al., 1996, Genomics 35:55; Cher et al., 1994, Genes Chromosom. Cancer 11:153; Bookstein, et al., 1994, Genomics 24:317; Akiyama et al., 1997, Cancer Res. 57:3548). Repetitive sequences were blocked by hybridizing 1-2 micrograms of amplified cDNA with an equal amount (by weight) of Cot-1 DNA (Gibco-BRL, Grand Island, NY) to achieve a final DNA concentration of 80 micrograms per milliliter in 120 millimolar $NaPO_4$ buffer at pH 7. Reaction mixtures were overlaid with mineral oil, heat denatured, and incubated at 60°C for 20 hours (Cot=20). Biotin-labeled genomic DNA samples were heat-denatured, loaded into Centricon™ 100 centrifugal ultrafiltration units (Amicon, Beverly, MA) together with blocked cDNA (1 microgram, excluding Cot-1 DNA), concentrated by centrifugation at 1000 × g for 25 minutes, and washed twice with 2 milliliters of 1 millimolar $NaPO_4$ buffer at pH 7. Samples were adjusted to achieve the following concentrations at pH 7: 120 millimolar $NaPO_4$, 1 millimolar EDTA, and about 160 micrograms per milliliter of DNA (excluding Cot-1 DNA). Reaction mixtures were overlaid with mineral oil and incubated at 60°C for 60 hours (Cot=120).

To prevent non-specific attachment of PCR-amplifiable cDNA to the beads, 10 microliters of an avidin-coated magnetic bead suspension (Dynabeads™ M-280; Dynal, Lake Success, NY) were mixed with 100 micrograms of sonicated salmon sperm DNA at room temperature for 30 minutes. The beads were pre-washed with TE buffer containing 1 molar NaCl, and were then incubated with complete hybridization reaction mixtures in 200 microliters of the same buffer at room temperature for 30 minutes. The beads were collected by using a magnetic concentrator (Dynal, Lake Success, NY), and the supernatant was removed. The beads were washed twice using 0.1 × SSC buffer supplemented with 0.1% (w/v) SDS for 15 minutes at room temperature, and were then washed three times using the same buffer at 65°C. Bound

cDNA was eluted from beads by mixing the beads with 100 microliters of 50 millimolar NaOH for 15 minutes and then neutralizing the mixture using 100 microliters of 1 molar Tris-HC1 buffer at pH 7.5. cDNA was purified using a PCR purification column (Qiagen™, Chatsworth, CA), per the manufacturer's instructions. cDNA was re-amplified by PCR using the same methods and the same conditions. The resulting amplified cDNA products were purified and blocked, and a second round of cDNA selection was performed as described herein.

Amplified cDNA was digested using restriction endonucleases *Sall* and *NotI*, cloned directly into pSPORT1 vector (Gibco-BRL, Grand Island, NY), and used to transform *E. coli* cells. CpG island cloning and shotgun sequencing were performed using this cDNA-containing vector. Using these methods, 87 potentially expressed clones were mapped in the YAC contig, as indicated in Figure 1C.

In CpG island cloning experiments, BAC DNAs were digested using restriction endonucleases *BssHII* and *SacII*, which specifically cleave CpG islands. After digestion with *Sau3AI*, the cleavage products were ligated into a pBK-CMV vector (Stratagene, La Jolla, CA), as described (Elvin et al., 1992, In: Techniques for the analysis of complex genomes: Transcribed sequences in YACs, Anand, Ed., Academic Press, London, p. 155).

Shotgun sequencing was performed as described (Inoue et al., 1997, Proc. Natl. Acad. Sci. USA 94:14584). Six hundred clones per BAC were picked and sequenced to identify candidate cDNA sequences. cDNA selection were performed for three YAC templates, as indicated in Figure 1C. Four hundred clones per YAC were picked up from the cDNA selected libraries, and all the clones were sequenced with vector primers. The sequences were analyzed using the BLAST computer software and the NCBI/BLAST database in order to exclude ribosomal or mitochondria-related genes. Fifty percent of clones were ribosomal or mitochondria-related genes, and the remainder were classified and were analyzed.

Two candidates CpG islands were identified from the region near marker *D8S233* by CpG island cloning. The BACs were partially sequenced by the

shotgun method to determine the presence of sequences matching expressed sequence tags (ESTs) in the nucleotide/EST database of NCBI/BLAST, and two ESTs from the BAC genomic region were thereby identified.

Using these approaches, a total of 123 clones 400-800 base pairs in length were selected and characterized, and 87 of those clones were mapped.

cDNA was synthesized using 2 micrograms of total RNA obtained from human brain, esophagus, or tumor cells or from 150 nanograms of poly(A)$^+$ RNA obtained from one of these cell types using the Superscript II™ plasmid system (Gibco-BRL, Grand Island, NY). The cDNA and an adaptor (Catalog #K1802-1; Clontech, Inc., Palo Alto, CA) were ligated to generate RACE templates, and the templates were used in PCR amplification of the cDNA. The chromosomal location of the *F37* gene was confirmed by identification of the presence of the *F37* gene sequence at 8p22 in a radiation hybrid panel designated Gene Bridge 4™ (Research Genetics, Huntsville, AL).

Full-length and 3'-truncated FEZ1 cDNAs were ligated to a expression vector pcDNA3HisA (Invitrogen, Carlsbad, CA) and cloned by RT-PCR, using human brain cDNA as a template. The entire nucleotide sequence of the insert cDNA was verified by DNA sequencing. The truncated cDNAs (nucleotides 1-1128 in the *FEZ1* ORF) lacked the portion of the ORF located 3'- with respect to the leucine zipper region.

In vitro transcription and translation was performed using a rabbit reticulocyte system (Quick TNT™, Pharmacia LKB Biotechnology Inc., Piscataway, NJ), and these reactions were monitored by PAGE. Full-length and 3'-truncated *FEZ1* cDNAs were ligated into a glutathione-S-transferase (GST)-fusion expression vector (pGEX ; Pharmacia LKB Biotechnology Inc., Piscataway, NJ), and the proteins encoded by those cDNAs were expressed, extracted, separated by PAGE, and visualized by Coomassie staining, as described (Ausubel et al., 1992, Current Protocols in Molecular Biology, John Wiley & Sons, New York). An image of the SDS-PAGE results is shown in Figure 2C. The protein in lane 1 of that SDS-PAGE was translated

from a pcDNA vector which comprised a truncated *FEZ1* cDNA lacking the portion of the cDNA located 3'- with respect to the leucine zipper region. The protein in lane 2 was translated from a pcDNA vector which comprised full-length *FEZ1* cDNA. The protein in lane 3 was translated from a pcDNA vector having no insert. The protein in lane 3 was translated from a pGEX vector which comprised a truncated *FEZ1* cDNA lacking the portion of the cDNA located 3'- with respect to the leucine zipper region.

The nucleotide sequence of the *FEZ1* gene open reading frame (ORF; exons 1-3) was analyzed in samples obtained from 194 cancer tissues, regardless of the whether or not *FEZ1* was expressed in the tissue. The sampled tissues were obtained from 72 primary esophageal cancers, 18 esophageal cancer cell lines, 24 primary prostate cancers, 3 prostate cancer cell lines, 39 primary breast cancers, 25 breast cancer cell lines, 8 primary ovarian cancers, 4 leukemic cell lines, and one cervical cancer cell line. Nucleotide sequence information was obtained by PCR and sequencing. Eleven pairs of PCR primers, as described herein in the Primer Nucleotide Sequence Table, were used to amplify *FEZ1* coding exons 1-3.

Genomic PCR was performed using the same conditions described herein for LOH studies, except that 4% DMSO (w/w) was added to the reaction mixture, and PCR amplifications were performed for 35 cycles, the additional 5 cycles being the same as the 20 cycles described herein. DNA sequencing was performed directly using the purified PCR amplification products. Sequencing reactions and analyses were performed by using the ABI Prism BigDye™ terminator reaction chemistry on the ABI Prism™ 377 DNA sequencing system (Applied Biosystems, Inc., Foster City, CA). Sequence data were confirmed by sequencing of duplicate PCR amplification products and by sequencing anti-sense strands using reverse primers.

The results of the experiments presented in this Example are now described.

Primary esophageal cancer tissue samples obtained from 23 of 53 patients (43%) exhibited loss of an allele at one or more loci on 8p, as indicated in Figures 1A and 1B. For example, tissue samples obtained from patient E26 exhibited

LOH at the markers designated *D8S264*, *LPL* and *D8S136*, and allelic retention at the marker designated *FGFR1*. Tissue samples obtained from patient E46 exhibited LOH at the markers designated *D8S264* and *D8S136*, and the markers designated *LPL* and *FGFR1* loci were homozygous, meaning that loss of an allele from one chromosome could not be detected if it occurred.

Of the 23 tumor samples in which loss of an allele was observed, 16 (70%) exhibited a commonly lost 1.5 megabase region located near the *D8S261* loci, and 14 of those 23 patients (61%) exhibited potential common LOH regions located near *D8S254*. These data suggest that two tumor suppressor genes are located in the chromosome region designated 8p22-23. The experiments described in this Example were focused on the more frequently affected 8p22 region around *D8S261*. This region is 4-6 megabases centromeric to the *MSR* region, and overlaps the target region in other tumors, including prostate and breast cancers (Kagan et al., 1995, Oncogene 11:2121; Macoska et al., 1995, Cancer Res. 55:5390; Jenkins et al., 1998, Genes Chromosom. Cancer 21:131; Yaremko et al., 1995, Genes Chromosom. Cancer 13:186; Yaremko et al., 1996, Genes Chromosom. Cancer 16:189; Kerangueven et al., 1997, Cancer Res. 57:5469; Anbazhagan et al., 1998, Am. J. Pathol. 152:815; El-Naggar et al., 1998, Oncogene 16:2983; Sunwoo et al., 1996, Genes Chromosom. Cancer 16:164; Wu et al., 1997, Genes Chromosom. Cancer 20:347).

In order to clone the genes present in this region, cDNA selection, CpG island cloning, and shotgun sequencing were performed. Using these procedures, 87 potentially expressed clones were mapped in the YAC contig, as illustrated in Figure 1C. RT-PCR amplification was used to select clones which exhibited reduced expression in tumor cells, and indicated that 43 of the 87 clones were expressed in normal adult tissues, including prostate. Nine clones showed reduced or no expression in cancer cells. Rapid amplification of cDNA ends (RACE) was performed, and the sequences of 6 of the 9 clones were extended successfully. Northern blot analyses indicated that expression of 5 clones was not remarkable in cancer cells. In contrast, RACE analysis using an *F37* clone, obtained by hybrid selection, indicated that a 6.5

kilobase transcript was expressed in non-cancerous tissues, but that the expression of *F37* could not be detected in the LNCaP prostate cancer cell line.

About 6×10^6 clones from a human testes cDNA library obtained from Clontech (Palo Alto, CA) were screened using probes specific for *F37*, and the nucleotide sequence of the 5'-end of the cDNA was obtained by the RACE procedures. The *F37* probe which was used had the sequence listed in Figure 5Q. The chromosomal location of the *F37* gene was confirmed by presence of the *F37* gene sequence at 8p22 in a radiation hybrid panel designated Gene Bridge 4 (Research Genetics, Huntsville, AL). These result indicated that the *F37* gene is located within 3.36 cR (centirads) of the genetic marker designated *WI-5962*. *F37* cDNA comprises a 1791 base pair open reading frame (ORF) which encodes a 597 amino acid residue protein having a molecular weight of approximately 67 kilodaltons. Homology searching of protein sequence databases indicated the amino acid sequence of *F37* comprises a leucine-zipper motif, and that this region has 32% identity (68% similarity) to the DNA-binding domain of a cAMP-responsive activating-transcription factor designated Atf-5 (Hai et al., 1989, Genes Develop. 3:2083). The homology search also indicated that the F37 protein has 38% identity to the protein designated KIAA0552, which consists of 673 amino acids (Nagase et al., 1998, DNA Res. 5:31-39).

Motif analysis software (Searching Protein and Nucleic Acid Sequence Motifs in Genome Net) predicted a cAMP-dependent phosphorylation site, located at Ser 29 of *F37*, and a predicted tyrosine-kinase phosphorylation site, located at Tyr 67 of *F37*. The ORF comprised three coding exons. The *F37* gene was designated *FEZ1* (F37/Esophageal cancer gene encoding leucine-zipper motif). The putative amino acid sequence of Fez1, the protein encoded by *FEZ1* is listed in Figure 2A. Nucleotide residues around the first methionine codon in *FEZ1* cDNA were matched using the Kozak recognition rule (Kozak, 1989, J. Cell. Biol. 108:229-241). a 5' in-frame stop codon was identified in the cDNA, located at -111 to -109 from the first methionine codon.

Northern blot analysis revealed that *FEZ1* gene expression was almost ubiquitous in normal tissues. *FEZ1* expression was most prominent in testes, as indicated in Figure 2D. *FEZ1* gene expression was analyzed by Northern blotting and by RT-PCR amplifications in human tumor tissue samples, including 41 cancer-derived cell lines and 25 primary tumors, as indicated in Figure 3A and summarized in Table 1. *FEZ1* expression was undetectable in 31 cancer cell lines (76%) and 16 primary tumor samples (64%). *FEZ1* expression was not detected in any of the 15 breast cancer cell lines studied or in any of the 10 primary breast tumor samples studied. However, *FEZ1* was expressed in normal tissues.

Table 1

Origin of Tumor Samples	Number of Cases Analyzed	Cases Expressing *FEZ1* mRNAs[1]	Cases with Aberrant Size Transcripts	
			Number of Cases	Case Names[2]
Esophagus Cell Lines Primary Tumors	 4 12	 1 9*	 1 4	 TE8 E16, E26, E41, E62
Gastric Cell Lines	 8	 3*	 Not Done	
Colon Cell Lines	 3	 2	 1	 SW480
Prostate Cell Lines Primary Tumors	 3 3	 2 0*	 1 -	 DU145
Breast Cell Lines Primary Tumors	 15 10	 0 0*	 - -	
Hematopoietic Cell Lines	 5	 1	 1	 MOLT4
Lung Cell Lines	 1	 0	 -	
Melanoma Cell Lines	 1	 1	 1	 G361
Cervical Cell Lines	 1	 0	 -	

[1] *FEZ1* Expression was detected by Northern blot or RT-PCR (indicated by *).

In E16, E26 and E41, normal tissues from a single patients' organs were analyzed, and did not exhibit alterations in the coding region sequences. In addition, the coding sequences from normal prostate as well as the other four samples from normal esophagus were analyzed, and no alterations were found except that one of twelve sequenced clones from testis cDNA showed a deletion of nucleotide.

In order to exclude the possibility that normal stromal cells, but not normal epithelial cells, might express *FEZ1*, *FEZ1* expression was assessed in normal breast epithelial cells and fibroblasts and in normal prostate epithelial cells (these three types of cells were obtained from Clonetics, San Diego, CA). RT-PCR amplification indicated that *FEZ1* was expressed in these three types of normal cells. No *FEZ1* expression could be detected in breast and prostate (LNCaP) cancer cells.

To exclude the possibility that the apparent differences in *FEZ1* expression observed among cell types might be attributable to alternative splicing of the *FEZ1* transcript, Northern blot analysis was performed using three different probes. The three probes were constructed to be complementary to a region of the ORF of the *FEZ1* transcript, complementary to a 3'-noncoding region just downstream from the ORF of the *FEZ1* transcript, or complementary to the 3'-noncoding terminal region of the *FEZ1* transcript. No difference was observed among Northern blots made using these three probes, suggesting that *FEZ1* expression was absent in the cell lines and tumors which were examined.

The nucleotide sequence of the *FEZ1* gene ORF was analyzed in a total of 194 cancer tissue samples, regardless of whether *FEZ1* was expressed in the tissue. These tissue samples included 72 primary esophageal cancer tissue samples, 18 esophageal cancer cell lines, 24 primary prostate cancer tissue samples, 3 prostate cancer cell lines, 39 primary breast cancer tissue samples, 25 breast cancer cell lines, 8 primary ovarian cancer tissue samples, 4 leukemic cell lines, and one cervical cancer cell line. Three point mutations were identified, two in two primary esophageal cancer tissue samples, and one in a prostate cancer cell line, as indicated in Figure 3B. These point mutations are summarized in Table 2.

Table 2

Tumor	Codon	Mutation	LOH at 8p22[1]	FEZ1 Gene Expression[2]
E44	29	TCC (Ser) → CCC (Pro)	+	Yes
E50	119	AAG (Lys) → GAG (Glu)	+	Yes
PC3	501	CAG (Glu) → TAG (STOP)	-	Yes

1 + means that locus D8S261 is observed; - means that a normal *FEZ1* allele was retained in at least a fraction of cells, as suggested by the results presented in Figure 3B.

2 Expression of FEZ1 was analyzed by RT-PCR in the two primary tumors or by Northern blot in the cell line.

In a primary esophageal tumor tissue sample designated E44, a point mutation resulted in an amino acid substitution of serine (normal) to proline (mutant) at amino acid residue 29. Amino acid residue 29 is, as described herein, a predicted cAMP-dependent kinase phosphorylation site. In another primary esophageal cancer tissue sample designated E50, a second point mutation resulted in a different amino acid substitution, namely lysine (normal) to glutamate (mutant) at amino acid residue 119. The LOH study described herein indicated that the two patients from whom samples E44 and E50 were obtained each exhibited allelic loss at the *D8S261* marker. Thus, tumor cells obtained from these two patients retained the mutated *FEZ1* allele and lost the normal *FEZ1* allele.

The third point mutation which was detected was a change of a codon encoding a glutamine residue in the normal *FEZ1* transcript to a stop codon at codon 501 in a prostate cancer cell line designated PC3. This mutation resulted in a *FEZ1* transcript which encoded a putative 166 amino acid residue protein lacking the normal carboxyl terminal region of wild type FEZ1 protein. Northern blotting, RT-PCR, and

nucleotide sequencing revealed that these three mutated DNA sequences were expressed in the patients and cells in which they were identified. These data suggest that *FEZ1* encodes a tumor suppressor protein, and that inactivation of *FEZ1* is involved in development of several common cancers.

The nucleotide sequences of cDNAs generated from mRNA expressed from *FEZ1* in several of the tumors were determined. Several internally-truncated transcripts were identified, as indicated in Table 3, Table 4, and Figure 3B. With one exception, *FEZ1* ORF sequences did not differ from wild type sequences in samples obtained from normal brain and prostate tissues (obtained from Clontech, Inc., Palo Alto, CA), from normal esophagus tissue samples obtained from seven individuals, or from matched normal cDNA obtained from patients E16, E26, and E41. One of twelve clones derived from testes cDNA samples (obtained from ClonTech Inc., Palo Alto, CA) exhibited a deletion at nucleotides 1441-1527 in the ORF. The cDNAs obtained from two esophageal cancer tissue samples exhibited a frame shift, with the result that the cDNA encoded a 76 amino acid residue protein.

Table 3

Tumor		Deletion[1]	Results[3]	Affected Exons	Putative Protein Coded in Frame[2]
E16		156-1542	FS	1, 2, 3	Zip(-)
E26		558-1715	IF	2,3	Zip(-)
E41		558-1715	IF	2, 3	Zip(-)
E62		558-1715	IF	2, 3	Zip(-)
TE8	a b	156-1542 1402-1578	FS IF	1, 2, 3 3	Zip(-) Zip(+)
DU145	a b	1366-1641 1402-1578	IF IF	3 3	Zip(+) Zip(+)
MOLT4	a	1402-1578	IF	3	Zip(+)
G361	a b	1417-1515 1516-1584	IF IF	3 3	Zip(+) Zip(+)

[1] The positions of the first and last nucleotides of deletions are shown according to the nucleotide number counted from first coding codon.

[2] Zip(+) means a protein comprising a leucine-zipper region; Zip(-) means a protein not comprising a leucine-zipper region.

[3] IF means that an in-frame region; FS means that a frame shift mutation was detected.

Table 4

	Deletion [1]	Donor Site[2]		Acceptor Site[2]
a	156-1542	TCCCAGGACTCCGGTCA(cggcaa (SEQ ID NO: 46)	...	gag)CGGCAAGGCCATGACCAG (SEQ ID NO: 47)
b	558-1715	AGCCTGCCCACACACAG(caccag (SEQ ID NO: 48)	...	cag)CGCCGGGGAGCCCTTGGA (SEQ ID NO: 49)
c	1366-1641	GTGAGAATGAGCTGCAG(cgcaag (SEQ ID NO: 50)	...	cag)CAGAGCTACGTGGCCATGT (SEQ ID NO: 51)
d	1402-1578	AGCTGCTGCGGGAGAAG(gtgaac (SEQ ID NO: 52)	...	cag)CATGAGCGGCTCGTGTGGA (SEQ ID NO: 53)
e	1417-1515	AGGTGAACCTGCTGGAG(caggag (SEQ ID NO: 54)	...	gag)CGGCTGCGGGCCGAGCTGC (SEQ ID NO: 55)
f	1417-1515	CTGCAGCGGGAGCTGGAG(cggctg (SEQ ID NO: 56)	...	gag)CGGCTCGTGTGGAAGGAG (SEQ ID NO: 57)

1-103-

[1] Nucleotide residues are numbered relative to the position of the first nucleotide residue of the first codon of *FEZ1* (i.e. residue 1).

[2] Nucleotide sequences flanking cDNAs deletion endpoints of are indicated. Upper case letters indicate nucleotide residues which are present in truncated cDNAs. Lower case letters in parenthesis indicate nucleotide residues not present in truncated cDNAs. Underlined characters indicate conserved nucleotide residues at donor/acceptor sites. The deletion in a results in a frame-shift which encodes a protein having a putative molecular weight of 8.6 kilodaltons.

The nucleotide sequences flanking deleted regions of *FEZ1* cDNAs indicated that the intronic AG sequence was present at the 3'-boundary of the deleted region in the cDNA, suggesting that the deleted *FEZ1* transcripts in tumors can be attributable to physiologically inappropriate splicing events. The allelic expression status of *FEZ1* was analyzed using a polymorphic site in the 3'-noncoding cDNA region, namely the 2134th nucleotide residue of *FEZ1* cDNA, numbered from the first nucleotide residue of the first codon. In four informative normal primary tissues, the *FEZ1* gene was transcribed from both alleles, i.e. it was not imprinted. In contrast, expression of *FEZ1* in *FEZ1*-expressing cancer cells was, in each sample studied, from a single allele, probably attributable to allelic loss.

Southern blot analysis of the *FEZ1* gene locus using an *FEZ1* ORF probe in 18 cancer cell lines indicated that one breast cancer cell line had a single rearranged *FEZ1* band and did not express the normal allele, as indicated in Figure 3C. No homozygous deletions were detected in the other 17 cell lines examined. Several tumor suppressor genes are associated with frequent allelic loss, and some are involved in homozygous deletions (Weinberg, 1991, Science 254:1138; Lasko et al., 1991, Ann. Rev. Genet. 25:281; Knudson, 1993, Proc. Natl. Acad. Sci. USA 90:10914; Nowell, 1993, Adv. Cancer Res. 62:1; Bookstein et al., 1997, Br. J. Urol. 79(Suppl. 1):28; Bova et al., 1996, Genomics 35:46; MacGrogan et al., 1996, Genomics 35:55; Cher et al., 1994, Genes Chromosom. Cancer 11:153; Bookstein, et al., 1994, Genomics 24:317; Ohta et al., 1996, Cell 84:587). These data suggest that, although LOH in the genomic region around the *D8S261* locus, as well as at the *FEZ1* gene locus, is a frequent abnormality, homozygous deletions of this gene are infrequent in tumors. Thus, the major mechanism of *FEZ1* inactivation appears to be attributable to "two-hit" events such as allelic loss and point mutations and, possibly, allele loss in combination with shut-down (i.e. null) transcription of the remaining allele.

The experiments presented in this Example demonstrate that loss of *FEZ1* function enhances tumorigenesis at least in prostate, breast, and esophagus

cancers, and likely in other malignancies associated with chromosomal alteration at 8p22.

Example 2

Effect of Fez1 Expression on Growth of Cells of Breast Cancer Cell Line MCF7

The Experiments described in this Example involve cells of the breast cancer line designated MCF7 (available from American Type Culture Collection, Gaithersburg, MD; accession number HTB-22) which were transfected with a vector which induces expression of *FEZ1* in the absence of tetracycline and represses *FEZ1* expression in the presence of tetracycline. Induction of *FEZ1* expression inhibited cell growth *in vitro* and *in vivo*.

MCF7 cells were stably transfected using a pTet-Off™ plasmid vector (ClonTech, Palo Alto CA; GenBank Accession number U89929) in which at least the coding portion of the *FEZ1* gene was operably linked with the tetracycline-responsive element and promoter of the vector. Cells were maintained in DMEM medium supplemented with 2 micrograms per milliliter doxycycline (Sigma Chemical Co., St. Louis, MO, catalog number D-9891) and 10% (v/v) certified fetal bovine serum (FBS; ClonTech). About 1×10^5 cells were grown in 3.5 centimeter diameter culture dish, and were transfected with about 4 nanograms of plasmid DNA using the GenePORTER™ reagent according to the supplier's instructions (Gene Therapy Systems, San Diego, CA), according to the instruction manuals.

Stable transfectants were made by maintaining transfected cells for about 2 weeks in medium containing hygromycin (Gibco, Grand Island, NY) at a concentration of about 200 micrograms per milliliter, beginning 36 hours after transfection. Four well-isolated transfectant clones were selected and designated clones 15, 18, 54 and 118. These clones were cultured in tetracycline-free medium comprising 10% (v/v) serum medium for 72 hours in order to induce expression of *FEZ1*. In the experiments described in this application, tetracycline and doxycycline were used interchangeably, because the tetracycline-responsive elements are substantially equally responsive to tetracycline and doxycycline.

Cellular proteins were extracted before and after induction of *FEZ1* expression, and separated by SDS-PAGE. Separated proteins were transferred to a nitrocellulose membrane, and immunoblot analysis was used to determine the presence of Fez1 protein or actin (as a control). A polyclonal antibody which binds specifically with Fez1 was used. The results of this immunoblot procedure are shown in Figure 6, and demonstrate that Fez1 protein was produced by each of the four selected clones when they were maintained in the absence of tetracycline. Fez1 protein was not produced by cells transfected with vector alone, indicating that there was no endogenous *FEZ1* expression in MCF7 cells.

Pub B13 The effect of *FEZ1* expression on *in vitro* cell growth of MCF7 cells was analyzed using the CellTiter 96™ AQueous non-radioactive cell proliferation assay obtained from Promega Corporation (Madison, WI) per the supplier's instructions. The absorbance of the MTS compound of the assay system at 490 nanometers exhibited a linear correlation between the number of MCF7 cells in a range between 10^2 and 10^4 cells, as confirmed by cell counting in which dead cells were excluded the dead cells by trypan blue staining. Cells of clones 15, 18, 54, and 118 were seeded in wells of 96-well plates containing tetracycline-free medium supplemented with 10, 5, 2.5, 1, or 0.5% (v/v) FBS. Culture medium was exchanged daily with the corresponding fresh medium. Absorption at 490 nanometers was assessed in order to estimate the number of cells present in each well at selected times. The results of these experiments are presented in Figure 7, in which data are shown as a ratio of the number of transfected cells to the number of control mock MCF7 transfectants (i.e. transfected with vector alone) cultured in the corresponding medium. Data were calculated as an average of four independent experiments, and bars in Figure 7 indicate standard deviations.

Figure 8 shows the results of a cell cycle analysis of synchronized transfected MCF7 cells. MCF7 transfectants were cultured in growth medium supplemented with 1.5% (v/v) FBS for 3 days in the presence or absence of tetracycline (i.e. in order to induce expression of *FEZ1* in cells maintained in the absence of tetracycline). Thereafter, the cells were maintained in medium comprising thymidine

in order to induce accumulation of cells at the G1/S stage of the cell cycle. The thymidine-containing medium was replaced with the same growth medium, and cells were fixed at selected times thereafter. The cells were fixed in 70% ethanol and treated with propidium iodide and RNase A prior to flow-cytometry analysis. Ratios were calculated as a ratio of the number of cells in the G2/M stage of the cell cycle to the number of cells in the G1 stage of the cell cycle (Figure 8A), or as a ratio of the number of cells in the S stage of the cell cycle to the number of cells in the G1 stage of the cell cycle (Figure 8B). The results of this analysis indicate that expression of *FEZ1* appears to inhibit MCF7 cell proliferation *in vitro* by causing accumulation of cells in the late S or G2/M stages of the cell cycle.

About 5×10^6 or about 2×10^7 cells (MCF7 cells transfected with the pTet-Off™ vector alone or MCF7 transfectant clone 15, 18, 56, or 118 clone cells) were subcutaneously inoculated into the left dorsal subclavicular region of 6 week-old female Balb/c nude mice. Four mice were used for each experimental group. Tumor volume was estimated for each mouse by measuring in two directions using Vernier calipers, and was calculated as tumor volume = length × $(\text{width})^2/2$. These results indicate that expression of *FEZ1* inhibited proliferation of MCF7 cells *in vivo*, and indicate that *FEZ1* expression inhibits (or even reverses) proliferation of epithelial tumor cells in animals.

Example 3

Construction of an Adenovirus Vector Having an Isolated Nucleic Acid Encoding at Least an Operative Portion of Fez1 Protein Incorporated Therein

Isolation of *FEZ1* cDNA

To construct an adenoviral expression vector, full-length *FEZ1* cDNA is isolated from human normal placental poly (A)+ RNA by reverse transcription polymerase-chain-reaction (RT-PCR) amplification using a pair of promoters, such as promoters having the nucleotide sequences,

5'-CAG ATG GGC AGC GTC AGT AGC CTC ATC-3' (SEQ ID NO: 58) and 5'-TCA GAT CTC AGT GGC TAT GAT GTC-3' (SEQ ID NO: 59).

Of course, any other pair of primers can be used to isolate *Fez1* cDNA, or the cDNA can be made synthetically, since the sequence is now available (Figure 5B; SEQ ID NO: 2; GenBank accession number AF123659). When the cDNA is isolated by RT-PCR, reverse transcription can be performed using the commercially-available SuperScript-II™ system (Gibco-BRL, catalog no. 18064-022, Rockville, MD) according to the supplier's instructions. PCR can be performed, for example, using Advantage Taq (Clontech, catalog no. K1905-y) according to the supplier's instructions). For example, reverse-transcribed cDNA can be subjected to PCR amplification by maintaining a standard PCR reaction mixture at 94°C for 30 seconds, and then performing 35 cycles comprising maintaining the reaction mixture at 94°C for 10 seconds, at 58°C for 10 seconds, and at 72°C for 60 seconds, and thereafter maintaining the reaction mixture at 72°C for 60 seconds.

The amplified product can be separated by electrophoresis in a 1.5% (w/v) agarose gel (Gibco-BRL, catalog no. 15510-019) as described in the Current Protocols in Molecular Biology, ed. Frederick M Ausubel et al., John Wiley & Sons, Inc 1987).

Poly (A)+ RNA can, for example, be purchased from Clontech (catalog no. 6518-1) and used to make cDNA. The Clontech poly (A)+ RNA material was extracted and purified from normal placenta tissue of Caucasian humans (ages 22-31) by a standard method described in Current Protocols in Molecular Biology (John Wiley & Sons, Inc.1987).

Adenoviral shuttle vector DNA can, for example, be obtained from Quantum company (Montreal, Quebec, Canada; e.g., pAdCMV-IRES-GFP, catalog no. AES050M).

Amplified *FEZ1* cDNA is isolated from an agarose gel and purified using, for example, a Qiagen™ PCR purification column (Stanford Valencia, CA; catalog no. 28104) according to the supplier's instructions. Adenovirus shuttle vector

DNA is digested using restriction endonuclease *Bgl*II (Boehringer Mannheim-Roche; Indianapolis, IN). After the ends of the DNA are blunted using, for example, T4 DNA polymerase (Promega, Madison, WI), 10 nanograms of cDNA is ligated with 100 nanograms of vector DNA. The resulting construct is used to transform an electrocompetent *Escherichia coli* strain, such as strain DH5a (Gibco), and the transformed cells are transferred to a culture plate containing LB agarose medium supplemented with ampicillin (e.g., as described in Current Protocol in Molecular Biology, John Wiley & Sons, Inc.1987).

Clones which contain *FEZ1* cDNA are selected, e.g. using a colony hybridization technique employing full-length *FEZ1* cDNA as a DNA probe (e.g., as described in Current Protocol in Molecular Biology, John Wiley & Sons, Inc.1987). These 'positive' clones are grown overnight in 5 ml of LB medium, and plasmid DNA is extracted from the positive clones, e.g. using a Qiagen miniprep column. The sequence of the extracted plasmid DNA can be analyzed at this point to confirm recovery of the anticipated construct. For example, sequencing reactions and analysis can be performed using the Applied Biosystems Prism™ BigDye™ terminator reaction chemistry and a Perkin-Elmer Gene Amp™ PCR system 9600 and the Applied Biosystems Prism™ 377 DNA sequencing system (Norwalk CT). After confirming the orientation of the cDNA strand within the vector DNA, the plasmid can be amplified in *E. coli*.

Confirming Transient Expression Using FEZ1 Adenoviral Shuttle Vectors

Promoter activity and adequacy of the plasmid vector can be checked by assessing transient expression of *FEZ1* in HeLaS3 cells (ATCC) maintained in F12/MEM medium supplemented with 10 % FBS. For instance, about 5×10^5 cells per cubic centimeter are grown in 6-well plate overnight. Three micrograms of plasmid is used to transfect the cells in each well, for example using a lipofection method (e.g. the GenePORTER™ Reagent, Gene Therapy System Inc.). After maintaining the cells under culturing conditions (e.g. for about 48 hours), the cells are harvested and *FEZ1*

expression is assessed, e.g. by immunoblot analysis using an anti-Fez1 antibody, as described in Current Protocol in Molecular Biology (John Wiley & Sons, Inc.1987).

The nucleotide sequence (SEQ ID NO: 60) of an adenovirus vector (designated pQBI-AdCMV5-IRES-GFP) into which an isolated nucleic acid encoding at least an operative portion of Fez1 protein can be incorporated is listed in Figure 10 and an isolated nucleic acid encoding at least a fluorescent portion of GFP.

Production of Recombinant Adenoviral Vector

Adenoviral vectors can be constructed in fetal kidney 293 cells (Microbix Biosystems Inc., Toronto, Ontario, Canada) by transfecting the cells with the adenoviral shuttle vector described above and adenovirus DNA (e.g. obtained from Quantum), as described (Miyake et al., 1996, Proc. Natl. Acad. Sci. USA 93:1320; Kanegae et al., 1994, Jpn. J. Med. Sci. Biol. 17:157). 293 cells obtained from Microbix Biosystems Inc. are low passages and would be adequate to obtain favorable homologous recombination efficiency. Transfected 293 cells are seeded in 96-well plate, and well-isolated plaques are selected.

293 cells can be transfected using the shuttle plasmid by the calcium phosphate precipitation method and grown in 100 millimeter diameter dishes. Twenty-four hours following transfection, the transfectants are seeded into individual wells of a 96-well plate (containing about 200 microliters of medium per well). The cells in the well are diluted with from about 10 to 100 times the number of non-transfected 293 cells. After 2 to 3 weeks of incubation, plaque formed cells are harvested and virus particles are extracted, e.g. by multiple freeze-and-thaw cycles. The number of plaque-forming wells is estimated to about 10-50 wells per 96-well plate.

The virus-containing supernatant obtained from plaque-forming wells is subjected to sequential infection of 293 cells in soft agar. For example about 5×10^5 293 cells are infected with 100 microliters of virus-containing supernatant, and the cells are seeded in 1.25% (w/v) low-melting temperature gel (Gibco) in a 60 millimeter diameter culture dish. After 10 days, plaques formed within the soft agar are isolated

under microscopic observation. For example, in a vector encoding green fluorescent protein (GFP), GFP can observed by fluorescence microscopy. Virus titers are propagated, for example by sequential infection of 293 cells grown in 75 to 175 milliliters of liquid culture medium in a flask.

Analysis of Expression of *FEZ1* in Cells Transfected Using the Adenovirus Vector

Expression of *FEZ1* in cells transfected using an adenovirus vector containing an isolated nucleic acid which encodes at least an operative portion of Fez1 protein can be detected by immunoblot analysis of proteins extracted from the cell, e.g. using a rabbit anti-Fez1 polyclonal antibody. For example, infectivity of the virus vector can be assessed by incubating HeLaS3 cells (ATCC) with an adenovirus vector-containing supernatant at a volumetric ratio of 1/40-1/10 (v/v), extracting protein from the cells, and assessing whether Fez1 protein can be detected by immunoblot analysis. Alternatively, if the adenovirus vector also encodes a detectable protein such as GFP, infectivity of the virus vector preparation can be assessed by assessing expression of the detectable protein in the cells incubated with the virus-containing supernatant. By way of example, if the adenovirus vector encodes GFP, infectivity of the virus vector can be assessed by detecting fluorescence in the cells at an excitation/emission wavelength pair that is characteristic of GFP.

Example 4

Identification of Fez1 Binding Partner Proteins

Yeast Two Hybrid Screening

Yeast two hybrid screening was performed in yeast strain Y190 using the MATCHMAKER™ system 2 (Clontech) according to supplier's instructions. We screened numerous clones of a human testes cDNA expression library individually fused with a GAL4 protein transcription activation domain-fusion pACT2 vector using a fusion protein comprising the GAL4 protein DNA binding domain fused with full length Fez1 protein. After first screening using a β-galactosidase assay, DNA was

extracted from positive clones and sequencing using vector primers in order to identify the cDNA clones.

In vitro Transcription/Translation, GST-Fusion Protein and *in vitro* Binding Assay

In vitro transcription and translation was performed using a commercially-available, rabbit reticulocyte-based system, (TNT™ T7 Quick Coupled Transcription/Translation System, Promega) by labeling with ^{35}S-methionine, according to supplier's instructions. GST-fusion proteins were isolated using a glutathione-agarose column (Pharmacia). Proteins were incubated in two binding buffers: buffer A (comprising 100 millimolar NaCl, 0.5% NP-40, 0.75 milligrams per milliliter bovine serum albumin (BSA), 20 millimolar Tris-HCl pH 8.0, and 1 millimolar EDTA) and buffer B (comprising 150 millimolar NaCl, 0.1% (v/v) Tween 20, 0.75 milligrams per milliliter BSA, 50 millimolar Tris-HCl pH 8.0, 5 millimolar EDTA, 10% (v/v) glycerol). After the glutathione-agarose beads had been pre-incubated in a 10% (w/v) BSA suspension, the beads were mixed with protein samples and washed 5 times, each wash comprising mixing the beads with 10 volumes of the binding buffer. After the beads had been washed, the bead-containing liquid was centrifuged to recover binding proteins. The samples were boiled for 3 minutes and then the proteins in the samples were separated by SDS-PAGE. The gel was dried and exposed to film for 4-24 hours at -80°C.

About 100 clones which encoded proteins that exhibited binding with Fez1 protein were identified. When the DNA corresponding to these clones was extracted sequenced, it was found that many positive clones were redundant. Several independent clones were identified, including clones encoding peptide elongation factor 1-γ (EF1-γ; cDNA sequence deposited by others as EMBL accession number X68142). EF1-γ is a member of microtubule-associated protein family. To confirm the result, β-galactosidase assay was performed, and EF1-γ exhibited strong interaction with Fez1. The reaction time was <15 minutes, compared with a positive control

reaction time of 15-20 minutes and a negative control reaction time of no reaction at >48 hours.

The results of an *in vitro* binding assay demonstrating binding between ^{35}S-methionine-labeled EF1-γ and Fez1 protein are shown in Figures 11A, 11B, and 11C. *In vitro* binding assay mixtures corresponding to lanes 1-8 contained *in vitro* translated EF1-γ protein. The mixture corresponding to lane 2 contained glutathione S-transferase (GST) fused with full-length (67 kilodalton) Fez1 protein, and the mixtures corresponding to lanes 4 and 7 contained GST fused with truncated (40 kilodalton) Fez1 protein. Mixtures corresponding to lanes 1, 3 and 6 contained GST protein (as a negative control). Mixtures corresponding to lanes 5 and 8 contained *in vitro* translated EF1-γ protein alone. The reproducibility of binding was confirmed by performing the binding assay in two different buffers, buffer A (lanes 1-5) and buffer B (lanes 6-8). The results of this experiment demonstrate that Fez1 protein and EF1-γ bind with one another.

Others have reported that the peptide elongation factors form a protein family, which is composed of at least EF-1α, EF-1β, EF-1γ and EF-1δ (J. Biol. Chem. 269:31410-31417, 1994; J. Biol. Chem. 269:2086-2092, 1994). We analyzed the binding of ^{35}S-methionine-labeled in vitro translated EFs to the GST-fused Fez1 protein (lanes 9-14 in Figure 11). No binding could be detected between Fez1 and either EF1-α or EF-1δ. An assay performed to detect binding of EF1-β with Fez1 was not informative, because EF1-β binds with GST.

Three ^{35}S-methionine-labeled deletion mutants of *in vitro* translated EF1-γ protein were made: a mutant designated EF1-γ(N) in which all but the amino-terminal 153 amino acid residues of EF1-γ were deleted, a mutant designated EF1-γ(C) in which all but the carboxyl-terminal 126 amino acid residues of EF1-γ were deleted, and a mutant designated EF1-γ(M) in which all but 149 amino acid residues in the central portion of the EF-1γ were deleted (i.e. EF1-γ(M) consisted of residues 154-302, measured from the amino terminus of EF1-γ). The amino acid sequence of EF1-γ can be found at GenBank accession number X68142. *In vitro* binding of these deletion

mutants with GST-fused Fez1 was analyzed. EF1-γ(N) bound with Fez1, but neither EF1-γ(C) nor EF1-γ(M) bound with Fez1.

In Vitro Binding Assay of Fez1 Proteins to the Amino-Terminal Portion of EF1-γ Protein.

The complementary binding assay was performed in buffer B using ^{35}S-methionine-labeled *in vitro* translated full-length 67 kDa Fez1 (lanes 1 and 2 in Figure 12) or truncated 40 kDa Fez1 protein (lanes 3 and 4 in Figure 12). The assay mixtures corresponding to lanes 2 and 4 of Figure 12 contained GST fused with EF1-γ(N), and the mixtures corresponding to lanes 1 and 3 of Figure 12 contained GST protein (as a negative control). *In vitro* translated full-length 67 kDa Fez1 protein (lane 5) or truncated 40 kDa Fez1 protein (lane 6) were loaded alone as controls. These results indicate that the amino-terminal 2/3 portion of Fez1 protein (40 kDa) binds with all or part of the 153 amino-terminal amino acid residues of EF1-γ *in vitro*.

Dimerization of Fez1 Protein *in vitro*

The amino acid sequence of Fez1 comprises a leucine-zipper-like region. Leucine zipper regions are known to be involved in the protein-protein and/or protein-nucleotide interactions in other proteins (Proc. Natl. Acad. Sci. USA 96:3928-3933, 1999). An *in vitro* binding assay was performed in buffer B, wherein the assay mixtures contained either ^{35}S-methionine-labeled *in vitro* translated full-length (67 kDa) Fez1 proteins (lanes 1, 2, and 5 of Figure 13) or ^{35}S-methionine-labeled *in vitro* translated truncated 40 kDa Fez1 protein (lanes 3, 4, and 6). The assay mixtures also contained either GST-fused full-length 67 kDa Fez1 (lane 2), GST-fused truncated 40 kDa Fez1 (lane 4), or GST protein (lanes 1 and 3; negative control). The results of these assays indicate that the 67-kDa Fez1 and truncated 40-kDa Fez1 proteins can dimerize.

Interaction of Fez1 with EF1-γ in Transfected Cells

Full-length FEZ1 cDNA was ligated with pcDNAV5 vector (Invitrogen, Carlsbad, CA) in order to express V5 tag-fused Fez1 protein in cells transfected with the vector. Full-length EF1-γ cDNA was ligated with pcDNAHis vector (Invitrogen) in order to express EXP tag-fused EF1-γ protein in cells transfected with the vector.

HeLaS3 cells were co-transfected with these two vectors using the lipofection method in order to analyze *in vivo* interaction between Fez1 and EF1-γ. Immunoblot analysis using anti-tag antibodies demonstrated that the transfected cells expressed V5/Fez1 fusion protein (lane 2 in Figure 14) and 50-kDa EXP/EF1-γ fusion protein (lane 8). Lanes 1 and 7 in Figure 14 represent vector control transfectant lysates, in which neither tag could be detected. A series of immunoprecipitation experiments (IP; lanes 3-6 and 9-12 in Figure 14) using anti-tag antibodies or control normal serum (NRS) was performed using the co-transfected cell lysate. Interaction of Fez1 and EF1-γ was indicated by precipitation of an apparently common band by anti-Fez1, anti-EF1-γ, and anti-V5 antibodies, as shown in lanes 4, 6, 10, and 12 of Figure 14.

Example 5

Making Antibodies Which Bind Specifically with Fez1 Protein

A rabbit polyclonal antibody which binds specifically with human Fez1 has been developed. Specificity of binding of the polyclonal antibody for Fez1 protein was demonstrated as follows. FEZ1 cDNA was ligated with a GST-fusion expression vector (pGEX, Pharmacia), and the protein was expressed in *E. coli* cells and purified. The Fez1-GST fusion protein was inoculated into rabbits to raise the anti-Fez1 antibody, which was harvested according to standard methods.

Figure 13A shows the results of an immunoblot analysis performed using the polyclonal anti-Fez1 antibody. About 100 (lanes 1-3) or 50(lanes 4-6) micrograms of protein obtained from human brain (lanes 1 and 4), testis (lanes 2 and 5), and spleen (lanes 3 and 6) were blotted onto a surface. Longer exposure of the film

showed faint expression of Fez1 in testis and spleen. Lane 7 contained *in vitro* translated full-length Fez1 protein, and lane 8 contained *in vitro* translated truncated Fez1 protein (i.e. lacking the C-terminal portion).

Figure 13B shows the results of an immunoprecipitation assay performed using the polyclonal anti-Fez1 antibody. HeLaS3 cells, which do not express *FEZ1*, were transfected with *FEZ1* cDNA ligated into expression vector pcDNA (Invitrogen) in frame with a V5 tag sequence. The cells were lysed, and the lysate was immunoprecipitated with polyclonal anti-Fez1 antibody (lane 1) or with the pre-immune normal rabbit serum (lane2). The precipitates were blotted and probed using the anti-V5 tag antibody.

Standard methods can be used to construct one or more monoclonal antibodies which bind specifically with Fez1 protein.

Example 6

Post-Translational Modification of Fez1 Protein

Cells of MCF7 clone 54 were cultured in tetracycline-free medium containing aphidicolin and either 10% (v/v) FBS or no FBS in order to synchronize cell cycles. At a selected time, the medium was replaced with aphidicolin-free medium with 10% serum, and the cells were incubated for the periods indicated in Figures 16A and 16B. Following the incubation, cell lysates were obtained, and the lysates were subjected to immunoblot analysis using the rabbit anti-Fez1 polyclonal antibody or with an anti-actin monoclonal antibody. The results of this experiment demonstrated that cellular Fez1 protein is post-translationally modified in a cell cycle progression-dependent manner.

Fetal kidney 293 cells (which express *FEZ1*) were maintained in serum-free medium containing aphidicolin in order to synchronize cell cycles. At a selected time, the medium was replaced with aphidicolin-free medium containing 10% (v/v) FBS, and the cells were incubated for the times indicated in Figure 17, after which incubation cellular proteins were extracted. The extracted proteins were subjected to

immunoblot analysis using rabbit anti-Fez1 polyclonal antibody or with an anti-actin monoclonal antibody. The results of this experiment are depicted in Figure 17.

The MCF7/Fez1 transfectant lysate which were used in the experiments for which results are depicted in Figure 16A were separated by SDS-PAGE in the presence of 6 molar urea. Under these separation conditions, only a single band corresponding to Fez1 protein was observed. Treatment of the same lysates with alkaline phosphatase (AP) resulted in formation of only a single band corresponding to FEZ1 upon SDS-PAGE separation. Treatment of the lysates with an AP inhibitor, β-glycerophosphate or a control did not lead to formation of a single band.

Cell Cycle Progression-Dependent *in vivo* Phosphorylation of Fez1

Cells of MCF7 clone 54 were cultured in medium which contained 2% FBS and aphidicolin for 2 days in order to synchronize cell cycle at G1/S. At a selected time, the medium was replaced with aphidicolin-free medium which comprised 10% FBS. Cells were harvested at selected times from 0 to 8 hours following replacement of the medium, and the cells were lysed to extract protein therefrom. The proteins were immunoprecipitated using rabbit anti-Fez1 polyclonal antibody, and the precipitated proteins were separated by SDS-PAGE. The separated proteins were blotted onto a surface and bound with either labeled anti-phosphoserine antibody (Sigma Chemical Co., St. Louis, MO; lanes 1-5 in Figure 20) or labeled rabbit anti-Fez1 polyclonal antibody (lanes 6-10 in Figure 20). The results of this experiment demonstrate cell-cycle dependence of Fez1 phosphorylation.

Example 7

Intracellular Localization of Fez1 Protein

Cytoplasmic and nuclear protein samples were prepared as the followings. Cytoplasmic and nuclear protein were isolated as described (DNA 7:47-55, 1998) with minor modifications. Briefly, about 10^7 293 cells were harvested and washed with PBS (10 millimolar $NaPO_4$ pH 7.4, 150 millimolar NaCl). After

sedimenting the cells, the packed cell volume (PCV) was measured and the cells were re-suspended in 3 PCVs of freshly prepared hypotonic buffer (10 millimolar HEPES pH 7.9, 0.75 millimolar spermidine, 0.15 millimolar spermine, 0.1 millimolar EDTA, 0.1 millimolar EGTA, 1 millimolar DTT, 10 millimolar KCl). The cells were allowed to swell for 10 minutes at about 0°C, and were centrifuged at 300 × g for 10 min at 4°C. The supernatant was collected as cytoplasmic extract I (C1).

The pellet was re-suspended with 2.9 PCVs of hypotonic buffer. The cells were broken by ten strokes using a Dounce homogenizer (Kontes Glass Co.). One volume of Sucrose restore buffer (prepared by adding 9 volumes of 75% sucrose to 1 volume of 10× salts) was added and was homogenized with 10 additional strokes of the homogenizer. The composition of 10× salts was as follows: 500 millimolar HEPES pH 7.9, 7.5 millimolar spermidine, 1.5 millimolar spermine, 100 millimolar KCl, 2 millimolar EDTA, 10 millimolar DTT. The homogenate was centrifuged for 30 seconds at 10,000 rotations per minute in a Sorvall HB-4 rotor (16,000 × g) at 4°C. The supernatant was collected as cytoplasmic extract II (C2).

The pellet was re-suspended in nuclear re-suspension buffer, using about 3 milliliters per 10^9 cells. Nuclear re-suspension buffer comprises 9 volumes of 20 millimolar HEPES pH 7.9, 0.75 millimolar spermidine, 0.15 millimolar spermine, 0.2 millimolar EDTA, 2 millimolar EGTA, 2 millimolar DTT, 25% (v/v) glycerol and 1 volume of a (4°C) saturated solution of ammonium sulfate. The re-suspended pellet was incubated for about 30 minutes at 4°C with occasional rocking. The extract was sedimented by centrifugation at 4°C for 120 minutes at 150,000 × g. The supernatant was removed, solid ammonium sulfate (0.33 grams per milliliter of supernatant) was added, and the sample was incubated for 20 minutes with occasionally rocking following dissolution of the ammonium sulfate. The sample was centrifuged at 85,000 × g for 20 minutes at 4°C. The pellet was dissolved in nuclear dialysis buffer, using 1 milliliter per 10^9 cells, and dialyzed overnight. Nuclear dialysis buffer comprises 20 millimolar HEPES pH 7.9, 20% (v/v) glycerol, 100 millimolar KCl, 0.2 millimolar

EDTA, 0.2 millimolar EGTA, 2 millimolar DTT). The nuclear extract (N) was stored at -80°C.

Forty micrograms of each of protein extracts C1, C2, and N by each method was separated by SDS-PAGE, transferred to a membrane, probed using either the rabbit polyclonal anti-Fez1 antibody (lanes 1-3 of Figure 21) or with an anti-tubulin antibody (Santa Cruz Biotechnology, Santa Cruz, CA; lanes 4-6 of Figure 21). The results of these experiments demonstrate that Fez1 protein is localized predominantly in the cytoplasm, although a fraction of Fez1 protein appears to be present in the nucleus.

Example 8

Interaction of Fez1 with Microtubules

Cytoplasmic protein fractions were obtained from Fez1-expressing 293 cells ("Tax" in Figure 22) which had been incubated with paclitaxel in order to polymerize tubulin and from Fez1-expressing 293 cells ("Col" in Figure 22) which had been incubated with colchicine for non-polymerization (i.e. as a control). The 293 cells were selected from three groups: non-synchronized cells ("non-treatment" in Figure 22), G1/S-synchronized cells ("0 h" in Figure 22), and S-to-G2/M-synchronized cells ("8 h" in Figure 22). The protein fractions were subjected to centrifugation in the presence of a sucrose cushion, as described (J. Cell Biol. 131:1015-1024, 1995). Pelleted proteins were subjected to immunoblot analysis using the rabbit polyclonal anti-Fez1 antibody. Protein remaining in the supernatant ("Sup" in Figure 22) were immunoblotted as well. The lower portion of Figure 22 demonstrates the presence of tubulin in all samples tested. The results of these experiments demonstrate interaction of Fez1 with microtubules *in vivo* and involvement of Fez1 with tubulin polymerization.

Involvement of GST-Fused Fez1 Protein with Tubulin Polymerization *in vitro*

Purified tubulin and microtubule-associated protein MAP2 were incubated at 37°C for 0-40 minutes with one of:

- GST,
- GST-fused Fez1
- GST-fused mutated (29 Ser → Pro) Fez1
- PKA-phosphorylated GST-fused Fez1 and
- PKA-phosphorylated GST-fused mutated (29 Ser → Pro) Fez1.

Polymerization of tubulin was assessed by spectrophotometric measurement of the increase in absorbance at 350 nanometers known to accompany polymerization. The results of this experiment demonstrate that Fez1 protein is able to inhibit polymerization of tubulin. The inhibitory effect of Fez1 protein on tubulin polymerization is modulated by the phosphorylation state of Fez1, as indicated by the effect of PKA-mediated phosphorylation of Fez1 on tubulin polymerization *in vitro*.

Example 9

A Proposed Biological Function for Fez1 Protein

It is recognized that the characteristics described herein for Fez1 proteins and nucleic acids which encode them do not depend on the accuracy or reliability of any theories presented in this Example with regard to the physiological function of Fez1 protein. Thus, without being bound by any particular theory of operation, the inventors propose the following biological functions for Fez1 protein.

Immunoblot analysis of extracts obtained from cells which express *FEZ1* demonstrates that Fez1 protein is predominantly localized in the cytoplasm, but is also found in the nucleus. Yeast two-hybrid screening demonstrates that at least one peptide elongation factor (EF1-γ) is a likely binding partner of Fez1 protein. Others have discovered that the EF family of proteins not only function as a peptide chain elongation factors, but are involved in interactions between microtubules and in the process of tubulin polymerization (see, e.g., Eur. J. Biochem. 171:119, 1988; Proc.

Natl. Acad. Sci. USA 90:3028, 1993; Plant Cell 6:893, 1994; Cell Motil. Cytoskel. 41:168, 1998). Other investigators have shown that EF proteins can determine susceptibility of cells to transformation (see, e.g., Nature 359:24, 1992). Overexpression of EF proteins has been observed in stomach, esophageal, and colon cancers (e.g., Cancer 75:1446, 1995; Gut, 38:66, 1996; Cancer 82:816, 1998). The results of experiments presented in this application demonstrate interaction between Fez1 protein and microtubules and their substituent proteins. For example, when cellular extract from Fez1-expressing cells was incubated with paclitaxel in order to induce tubulin polymerization, Fez1 was determined to be associated with tubulin precipitates. However, Fez1 was determined not to be associated with depolymerized microtubule precipitates in the presence of the tubulin polymerization inhibitor colchicine.

The data presented in this application indicate that Fez1 protein serves to modulate polymerization and stability of microtubules, and possibly other cytoskeletal features, *in vivo*. Thus, Fez1 protein can be expected to be involved in cellular processes which are modulated by cytoskeletal stability and changes. Examples of such cellular processes include initiation of mitosis, modulation of the rate and stage of mitosis, modulation of the initiation and rate of cell proliferation and growth, modulation of cell shape and rigidity, modulation of cell motility, modulation of the rate and stage of cellular DNA replication, modulation of the intracellular distribution of organelles (e.g. mitochondria, endoplasmic reticulum, Golgi apparatus, chloroplasts, and the like), modulating the metastatic potential of a cell, and modulation of cellular transformation from a non-cancerous to a cancerous phenotype.

For example, cell division of higher eukaryotes is known to be initiated and be regulated according to a dynamic process, which involves the so-called mitotic apparatus (an organized complex of proteins) that distribute the duplicated chromosome to daughter cells (see, e.g., Nurse, 1990, Nature 344:503-508). The extended microtubular cytoskeleton of an interphase cell is disassembled into tubulin subunits, and, when an appropriate point in cell cycle occurs, the tubulin subunits are

re-assembled into two sets of polarized spindle tubes, that function as a central part of the mitotic apparatus. Once nucleation of spindle tubes occurs, the growing tubules attached at an end of a condensed chromosome. At the other end, the tubules meet or attach at a collection of proteins designated the centrosome or microtubule organellar center. The centrosome complex has been isolated by others (see, e.g., Telzer, 1979, J. Cell Biol. 81:484-497; Mitchison, 1984, Nature 312:232-237), and previous reports characterized soluble protein precursors of the centrosome. The centrosome comprises α-, β- and γ-tubulin, heat shock protein 70, and an elongation factor protein (Eur. J. Biochem. 171:119, 1988; Proc. Natl. Acad. Sci. USA 90:3028, 1993; Plant Cell 6:893, 1994; Cell Motil. Cytoskel. 41:168, 1998).

As a normal cycle of cell division progresses, both disassembly and re-assembly of microtubules occurs. Thus, some gene product or reagent, which targets microtubules or their subunits, can be used to modulate progression through the cell cycle. Tubulin is a target for known anti-cancer drugs, such as paclitaxel (which can induce tubulin polymerization) and *vinca* alkaloids (which can inhibit polymerization process; Med. Res. Rev. 18:259-296, 1998). Other known tumor suppressor genes have been shown to be involved in the dynamics of microtubule assembly and disassembly. For example, APC can promote microtubules assembly (Eur. J. Biochem. 253:591, 1998; Cancer Res. 54:3672, 1994). Fhit can induce microtubule assembly (J. Biol. Chem. 274:34, 1999). As demonstrated herein, Fez1 can inhibit tubulin polymerization. Because, as demonstrated herein, Fez1 binds with at least one EF protein, and because these proteins have been identified as a soluble protein component from the centrosome, it can be expected that Fez1 has an role in the late events of the cell division process or centrosomal dynamics. This is in keeping with the finding herein that Fez1 protein induces accumulation of cells in the late S to G2/M stage(s) of the cell cycle. In these stages the centrosome is undergoing assembly in daughter cells.

The experiments described herein demonstrate at least two ways in which the activity of Fez1 can be affected, namely by phosphorylation of Fez1 protein and by binding a polypeptide or polypeptide-like molecule with Fez1 protein. The

results presented herein demonstrate that phosphorylation of Fez1 by PKA can diminish the ability of Fez1 to inhibit tubulin polymerization.

Agents which directly phosphorylate Fez1 or which induce its phosphorylation or inhibit its dephosphorylation by other proteins are useful for diminishing the ability of Fez1 to inhibit tubulin polymerization and corresponding growth/shrinkage and maintenance of cytoskeletal features (e.g. microtubules) which contain tubulin or tubulin-like proteins. Agents which directly dephosphorylate Fez1 or which induce its dephosphorylation or inhibit its phosphorylation by other proteins are useful for enhancing the ability of Fez1 to inhibit polymerization and corresponding growth/shrinkage and maintenance of cytoskeletal features which contain tubulin or tubulin-like proteins.

Agents which are able to bind specifically with Fez1 protein can also modulate its physiological activity. Examples of such agents are antibodies which are raised against Fez1 protein, tubulin, and EF1-γ. Fragments of such proteins (e.g. Fc portions of antibodies or the EF1-γ(N) fragment described herein) can exhibit effects on Fez1 protein that are similar to the effects of the whole protein on Fez1 protein. Similarly, peptide or peptidomimetic compounds which mimic the structure of the portion of a protein that binds specifically with Fez1 protein can exhibit effects on Fez1 protein that are similar to the effects of the corresponding whole protein on Fez1 protein. The inventors recognize that numerous methods known in the art can be used to construct and screen libraries of compounds which are structurally similar to proteins that bind specifically with Fez1 protein (e.g. peptide or peptidomimetic compounds which are structurally similar to one or more portions of tubulin, EF1-γ, or an antibody that binds specifically with Fez1). In addition, the observation herein that Fez1 protein appears to form dimers or multimers indicates that compounds which are identical to or which mimic the structure of a portion of Fez1 involved in dimerization or multimerization can also be used to modulate the physiological activity of Fez1. Thus, methods of constructing and screening libraries of compounds which are identical to or structurally similar to a dimerization/multimerization domain (e.g. a

library including random fragments of Fez1 protein) can be used to identify compounds which modulate the physiological activity of Fez1.

The disclosure of every patent, patent application, and publication cited herein is hereby incorporated herein by reference in its entirety.

While this invention has been disclosed with reference to specific embodiments, it is apparent that other embodiments and variations of this invention can be devised by others skilled in the art without departing from the true spirit and scope of the invention. The appended claims include all such embodiments and equivalent variations.